

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCC
CAGCGCTACCGGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTTAACAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCCGCTGTCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGCACTTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGTGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGTCTCTCCAGGAACCTACCGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGTGCCACATGGGGTACCAGGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGTCTCGGGCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGTACCGCAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAACCTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCTCCTGACGGCTTCGAAGAAACG
GAAGATGCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTATAGTGCCGGCACTTACCCTTTAAATATTTCAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTCTACTGCATTCTAGTTGGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

090697-071201

097076

><MW: 38192, pI: 4.53, NX(S/T): 2

Signal peptide:

N-glycosylation sites.

Glycosaminoglycan attachment sites.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation sites.

Tyrosine kinase phosphorylation site.

N-myristoylation sites.

Aspartic acid and asparagine hydroxylation site.

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCACCGCTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACA
 GCCTTGCTGAGGGAGCTCGACGCGAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
 GCACGAGGAGTTTTCCCGCGAGCGAGGAGTCTCTGAGCAGCATGGCCCGGAGGAGCGCCTTC
 CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCTGCTGGCACTGCGGCGGAGGCG
 CGGGCCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
 TAGGATTTTGAAGAAGATATCTCTGATTGTTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
 TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
 CTGGCAAGCTGCAGGGCAGGCGAGAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGATA
 AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCCTCACAAGGCA
 TCAGTTGTTCAAGTTGTTTCCCATGTCTTGGAACACAGGATGGGGTGCCAGCATTTGAAGT
 GGATGTGATTGTTATGAATCTGAAGGCAACACCATTTCTCCAAACACCTCAAAATGCTATCT
 TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
 GAAAGACGCACTGCGAGTGTCTGTATGGGTTCCACGGACCTCACTGTGAGAAAAGCCCTTGT
 TACCCACGATGTATGAATGGTGGACTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTGT
 GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGTCAACCACCTGCTTAAATGGAGGGACC
 TGTTTCTACCCCTGGAAAAATGATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAG
 CAAATGCCACAAACCTGTGCAAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGT
 CCAAAGGTTACCGAGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT
 GGAACCTGCCATGAACCCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACATGCAAC
 TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCGACCTCAGGCA
 ACACGCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCACCTGAATCCAAATACATCTGG
 TGAACCTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTTCATAGCCTTTGTTAACTTTCA
 TGTGTTGAATGTTCAAAATATGTTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
 TCATTATAAAATCACGTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGCTGTAG
 CATGATGGTATAGATTTTCTGTGTTTCACTGCTTTGGGACAGATTTTATATATGTCAATTGA
 TCAGGTTAAAAATTTTCACTGTGTAGTTGGCAGATATTTTCAAATTAACATGCAATTTAGGT
 GTCTGGGGGCGAGGGAACATCAGAAAGGTTAAATTTGGGCAAAATGCGTAAGTCAAGAAT
 TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGAGATTTTAGAT
 GTTGTGTACATTTTAAAAAATTGCTCTTAATTTTAAACTCTCAATACATATATTTTGACC
 TTACCATTTATCCAGAGATTCACTATTAACAAAAAATTAACATGTGGTAGTGGCATT
 AAACAATATAATATTTCTAAACACAATGAAATAGGGAATATAATGTATGAATTTTGTGAT
 TGGCTTGAAGCAATATAATATATTTGTAACAAAAACACAGCTCTTACCTAATAAACATTTTAT
 ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTGGAAAAAATAAATAAATAA
 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
 CGCCATGCCCCAATTTGTTTATTTGAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAALWLWSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQGVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICCPPGLEGEQCEISKCPQPCRNGGKICIGSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHPEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGACAGCCAGGAGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCACACCTTCACCAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCGG
GAGCTAGCACC GGGTCTGCACCTGCGGGGCATCCGGGACGCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTTCGTATCTA
TCCAGTCTTTGGGAACGTACTGGGACAACGTGTAACCGTGCACCTGCCAGGAGAACAGGCCAT
GGCATGTGGTATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCAAGCGCCTTCTGGGGCATGACCTGGATGAAGGGGCACTTCGCTACCGCCTGGGCACCA
TCCGCCCATCTTCTCGGTGATGAACATGCATGAAATTTATACAGTGTGTAACCCAGGGGAG
GTGCTTCCACAGCCTTCCAGGCGCTCTGAGAAGTGGCCCAACCTGATTTCATGAGCCTCTTGA
CCAAGGCAACTGTGACGGCTCTCGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCCCAGAACCCTGTGTCTTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGCTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCCAACAGCTATGTTAATAACAAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGGCACTTCCGCATCGTGC GCGCGTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG
CGGGCACCAACGCGGGTCCGCGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGCGCGGGTTCGCTGACGACGCGCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCCAACCCAAATCCCGTATTCTTTTTTTTTTTTTTTTATAGACAGGTCTTGTCTCCG
TTGCCAGGTTGGAGTGACGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
AGTGACCTCCCACTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACTGGC
TAAATTTTGTATTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAATC
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCCTCCCAAAGTGCTGGGATTGCAAGGCATGAGCC
ACTGACCCAGCCCTGATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTWYDNCNR
CTCQENRQWHGGSRHDDQSHQPGQLWLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

0904877.071204

FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCAGGTGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAC TGCGTGG ATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACTGGGTGTGGTGCCCCAGGCCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGGTTCTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCCTCTCTGCTGCTGTTT
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGCAGGCACTCAGGAGGGCCAG TAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLP PPSLRCSLHSACCSGDFASYRLWGAPLQPT
LGVVPQASVPLLLTDLAQWEPVLVPEAHPNASLTMVCTPVPHDPFPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPFAFSTLNFVLRLHLPQEAFPAHPIYDLSQVWSVVS PAPS R GQAL RRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCG~~AT~~GGGAGCGCCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTAGGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAAGTACACGGGCGTGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTGCGATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAACATATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTTCATGGCCTTACACGCGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCCGCAGAAC
CAGCGCGAGGCCCCTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGAACCAAGCGCACAC
GGCGGCCCCAGCCCCCTCAGCTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGCCCGGTG
CCCCAGGGGCGGTGGCAGTGCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTCAACCTGATCTCAGGCCACCGCCTCTGCCGCCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTGAGCGACTGAAGGCCTTGACAGACAACCGCTTGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAAAACCTCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTGTTGTTTTCAGGAAAAAGAAAGGAGAGAGGAAAATAG
AGGGTTGTCCACTCTCACATTCCACGACCCAGGCCTGCACCCCAACCCCACTCCAGCCC
CGGAATAAAACCATTTTCTCTGC

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FIGURE 11

MGAA RLLPNLTLC LQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLIGKPSGKSKDCVFT EIVLE
NNYTAFQONARHEGWMAFTRQGRPRQASRSRQNR EAHFIKRLYQGQLFFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCCTCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGGAGATTTATTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTCTTTTCCCACCACATTGTATTTTAT
 TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGGCCAGCCATGGGGCTTTTTCTCT
 GAAGTCTTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCTGGCCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCAGAGCTTGACCTCAGTG
 CCTCTTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC
 TGGATTTCCCTGCAGAACTGCACAATGTACAGTCCGTGTCACAGGTCTACCTGTATGGCAACC
 AACTGGACGAATCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTGTCAGGAAAAAC
 AATATTACAGACCATTTACGGGCTGCTCTTGCCTCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGTGACAACCTCCATATCCACAGTGGGGTGGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
 TCAAAATGTTGTTTTGTCTAAGAAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTGCATATCCGACATGGCCCTTCCAGAA
 TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAGGGGTATCGCGG
 AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCAATTGTACGTAATTCGCTGTCC
 CACCCTCTCCCGATCTCCACGGTACGCATCTGATCAGGCTCTATTGTCAGGACAACCAGAT
 AAACCACATTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGTATACTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCTTTGGTTTTGTGACTGACGATTAATAATGGGTCCACAGAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTTCATGTGCCAAGGTCTGAAACAGTCCGGG
 GGATGGCCGTGAGGGAATTAATATGAATCTTTGTCTGTCCACACAGCCCCCGGCTG
 CCTCTCTTACCCACAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTAT
 TCCAAACCTTAGCAGAAGCTACACGCCCTCCAACCTCTACCAATCGAAATCTCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCCACTATTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTTCCACGTGATGGCATA
 CAAACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACCATTTGTTAGAGGC
 CACCACCATGCTCTCTATCTGAACAACGGCAGCAACAAGCTCCAGCCATGAGCAGACGA
 CGTCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
 CCAGAAGTGAAAATACAACCGGGCCGGCGGAAAGATGATTATTGCGAGGCAGGCCAAGA
 AGGACAACCTCCATCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCTTAAATAACGAT
 CAACTCTTAAAGGAGATTTCAGACTGCAAGCCATTACACCCCAATGGGGGCATTAAATTA
 CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGAC
 ACTGCCATACGTCAGAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGAGATTACATTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTTCTATTCAAGTTAATTACAAACAGTTTTGTAACCTTTTCTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelhNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAISLKLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGGPEQVRGMAVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHEGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKGRYTSQWKYNRGRKKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLK
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGCTCGCCTCCCAAGAGCG
ATCCCCGAGGAGAGCGCGGCCCTTCGGCGAGGCGCAAGAGGCCGACGAGGAAGACCCGGTGGCTGGCGCCCTGGCC
TCGCTTCGCCAGGCGCGCGCGCTCGAGCCTTGCCCTCTTGCTCGCCTTGAAAATCGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCTTCGACAGATCGTCTCTCTCTCGGAGCGAGGACGGTCACTGCGGAGGTCATCT
CTAGGGGCGAGCACGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTTCTCTGGAGAACAGCGGGCAGAGCC
TGGTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTTCATCGTGAGCA
CTCTTGCAATTCTTGACATTGGTCTGATGTACCCGAGTGGGCTGCTCCAATATGGCAGCAGCTGTCAAGAAATG
AGTTTCTCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTCTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATCATGTGGCTGGCCATCCAGTATGCGCTGAACATCGCATTTCTCAGAAAGCAGAGGGGCGCCGGCCCTGA
GGGAGAAATGTGCCACGGGTCTAATATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCAGAGGTGGCTGCTA
AGGACCGGACACGGGCACTCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGCTTCTTGTGTGGCAATTTGAGCCAGATTGAGACGCTGACCTCCGTGTTC
AGAAGAAGTTGTGACCGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATAGTCTGACGGTGCACAAAGGCTACATTTCTCACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT
GTGCCATGGAGGCCAACATGTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCCTTCGCTCGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCTCAGACCTCAGGATGTGAAC
ATGAGTGTGTAAATGTGGCTGCGCTTCTTGTGCCAGTGCATGAAGGATTTGTCTTAAACCCAGATGAAAAA
CGTGACAAAGGATCACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGAGGAGAGCT
ACTACTTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCATGTGCGAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTTCTTCGCTCGCCAGTGCTCAGAAAGCTTCC
TCATCAACGAGGACCTCAAGACCTGTCTCCGGGTGGATTACTGCTGTGAGTGACCATGGTTGTGAATATCTCT
GTGTCAACATGGACAGATCTTTGCCCTGTGAGTGTCTGAGGGACACGCTGCTCCGACGCTAGGGAAGACGTGTG
CAAAATTTGGACTCTTGTGCTCTGGGGGACACCGGTGTGTGAACATTCGTGTGTGAAGCAGTGAAGATTTCGTTGTGT
GCCAGTGTCTTGAAGTTATATATCTCCGTGAAGATGGAACAACTTGCAGAGAGGAAGATGTCTGCCAAGCTATAG
ACCATCATGCTTGTGCTTATTTGTGTGAACAGTGAACGACTCATACGCTGCAGGTGCTTGGAGGGATTCGGCTCG
CTGAGGATGGGAACCGCTCGGAAGGAAGGATGTCTGCAAAATCAACCACCATGGCTGCGAACACATTTTGTGTTA
ATAATGGGAATTTCTACATCTGCAATGTCTCAGAGGATTTGTCTACAGTCAGGACGGAAGACCGTGCACAGAAAT
GCACTGAAGGCCCAATTTGACCTGTGCTTTGTGATCGATGGATCCAAGATCTTGAGAAAGAGAAATTTGAGTGG
TGAGACCAATTTGTCACTTGGAATTAATAGATTCTTGACAAATTTCCGCCAAGCGCTCGAGTGGGGCTGCTCCAGT
ATTCTCZACAGGCTCZACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC
ACXTGAAATACATGGGAAGGGCTCTATGACTGGCTGGCCCTGAAACACATGTTTGAGAGAAAGTTTATCCCAAG
GAGAAGGGGCGAGGCCCTTTTCACAAAGGTCGCCAGAGCAGCCATTGTGTCACCGACGGAGCGGGCTCAGGATG
ACGTCTCCGAGTGGGCGAGTAAAGCCAAAGGCCCAATGGTATCACTATGTATGTCTGTTGGGGTAGGAAAAAGCCATTG
AGGAGGAACACAAAGAGATTGCTCTGAGGCCCAACAAACAGCATCTCTTCTATGCGCAAGACTTCAGCACAAATGG
ATGAGATAAGTGAACAACTCAGAAAGAGGCATCTGTGAAGCTCTAGAAGATCTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACCTGCCAAAAACCGTCCAACAGCCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAAGCCTATT
CTGTGTTCTAATTTTCAGTGCAACACAGATATCTGTTTGAAGAAGACAACTCTTTACCGGTCTACACAAAGCTTT
CCAGTCAACAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGAGATGTGAAACCTTATAATGT
TCCAGAACCTTGCAACGGAAGAGTAAGAAAAATTAAACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAAATCGCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCAATGTATCACGGATTACAAT
GAACCGAGTGCAGAGCCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA
GAAACCTGGTTTGCACAGAAACAAAGACAGAAAGTATACACTAATTTGATATAAAATTTATCTAGGAAAAAAATCTC
TCAGAAATTTAAGATGAATTTACCAAGTGAGAAATGAATAAGCTATGCAAGGATTTTGAATATCTGTGGACAC
AACTGCTTTGCTCATCTTACGCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGACAGTCTTCACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTACCTTGATATATGATATGGATGTATG
CATAAATCATAGACATATGACTCTGTGGAACAGTTGGATTTTTTATACAATATAAAAATCACCACTGAG

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FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFNSQIETLTSVQKKLCTAHMCSTLEHN
CAHFICINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASNHGCEHECVNADGSYLCQCHEGFALNPDEKCTRINYCALNKPQC
EHECVNMEESSYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLFI
NEDLKTCSRVDYCLLSDHGCEYSVNMMDRSFACQCPGHHVLRSDGKTCALDSCALGDHGC
HSCVSSSEDSFVCQCFFGYILREDGKTCRRKDVCAIDHGCEHICVNSSDSTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEBLQEIASEPTNKHLYFAEDFSTMDIEISEKLKKGICEALEDS DGRQDS
PAGELEPKTVQOPTSEPVITINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSP
BEKHQCKCENLIMFQNLANEVVRKLTQRLEEMTQRMALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGT CAGCGGCTCGGCTCCCGCGCAGCTCCGGCCGTGCGCGAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTTGCCCCCAACCGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCTCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGAACCTGCCCCGAGGCTCAGACACAATCTCCAAGAATGGGACCTT
TTCCTCTGTCACTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAGACTGCCACGACAGAT
GGGGCCACCCCTAACCAATATCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCCAGAGTCAAGCTGGCTCTCTGGTAT**TGA**TGAC
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCTCTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTGCAAATTTAAATAAAGATACATAA
TGTTGTATGAAAAA

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FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGFPY
SCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPHVGANVTLSQCQSPRSKPAVQYQ
WDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPFRPGALTTPSLSSQALPSPRLPTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

CGCCACCCTGCGGCLACCGCCAATGAACGCTCCCGCTCTAGTGGTTTTTCCACTTTG
TTGAATTTGTTCTATATCAAAATTGCAACAAGACACCTTGCTCCCAAATGCAAAATGTGA
AATACGCATTCGAATTTGAAGCTGCTATTGCAACATGGGATTTTCAGGAATGGTGTACAA
TTTTGTGAAGATGATAATGAATGTGAAATTTAACTCAGTCTCTGTGGCGAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGATGTGTACTGGCTTCAGATCCAGCGAGTAAACA
ACGAGGTTTCTCACTAATGATGAAGCCGTCTGTATAGAAATGTGAATGCAAACTGCCATT
TAGATAATGTCTGTATGCTGCAAAATTTAATAAAACTTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTTTGCTACAAGAAGCTATAGAAATTTGTGACAGCATTTTCCACAACAG
TATAATTACATATATAGAAATTTAGTGTGAATCATCTTCAGTCTAGGTTACAAGAACAAC
CATCTCCAGCACAAGGACACCTTTTAACTCAACCTCTTACTGAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGATACATTTTGTAGTTTGGGACAAGTATTCTGTGAATCATAGGAGAAC
ACATCTTACAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACACAGAGTTTGTATACAAATTCACCGGATATAGCTCCAAAGTTTCTTTTGTGAT
TCATATAACGATGAACATATTCTCATCTGAATGAATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCTATATGATTCAAATGGCAACTGTTGCAGTTGCATTTTATATATA
AGAGTATTGGCTCTTGCTTCATCATCTGCACACTGTTCTTATGAAACCTCAAATTTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGCTCTCAATAGAGCTCAAAACC
ACCCACATATATATGAACCTTGAATAAAATAAACATTACATTAAGTCATGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCATTTTGAATTTACTCACTGATACCATGAAAGTGGCAGTGGTCT
TCAGAGGGCTGTGAGCTGACATATCAAATGAGACCCACACCTCATGCCGCTGTAAATCACCT
GACACATTTTGAATTTTGAATGTCTCTGTGGCTTCCATTTGGTATTAAGGATTTAATATTTCT
TTACAAGGATCACTCAACTAGGAATAATTAATTTCACTGATTTGTCTGTCATATGATCACTTTT
ACCTTCTGTGTTCTTCAGTGAATTCACAAAGCAGGACAACAATTCACAAAATCTTTGTGTG
TAGCCTATTTTCTTGCTGAACCTGTGTTTTCTGTGGGATCAATACAAACTAATAAGCTCT
TCTGTTCAATCATTTGCCGGACTGCTACACTACTTTCTTTAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCATCTCAATTTGTGTGGGTGTCACTACAAACAGGGATTTTGCA
CAAGAATTTTATATCTTTGGCTATTGAAGCCAGCCGGTGTAAGTTGGATTTTCCGACAGCA
TAGGATACAGATATTATGGCACAAACCAAAGTATGTTGGCTTAGCACCGAAAACAACCTTTATT
TGGAGTTTTTATAGACACAGCATGCCTTAATCATCTTGTTAATCTTTGGCTTTTGGAGTCAT
CATATAACAAAGTTTTTTCGTCACTCGAGGTTGAAACAGCAAGTTAGTGCTTTTGAGAACAC
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTCTCTGCTTCTCGGCACAGCTGGATCTTT
GGGCTTCTCCATGTTGTGCGCATCAGCTGGTTAGCTTTACCTCTTCACAGCTGCATCTTT
TTTCCAGGGGATGTTCAATTTTTTTTATTCCTGTGTGTTTTATCTGAAAGATTCAAGAAGAA
ATTACAGATTTGTCAAAAGTGTCCCTCGTGTGTTTGGATGTTTAAAGTAAACATAGAGATT
GTGATAATTCAACTGCACAAAATAAAAAATCCAAGCTGTGATGACCAATGTATAGAAATG
TGACTCATCAAATTAATCCAAATTTAACTACTAGACAAAAGTATTTTAAATCAGTTTTTCT
TTTTTGCTGATAGGAACGTGTAGATAATAAGTAAAAATGTATCATATAGATATACATATGT
TTTTCTATGTGAATAGTTCTGTCAAAATAGTATGCGAATTTTGGAAAGTAATTTGGTTT
CTCAGGAGTGATATCACTGCACCCAGGAAAGATTTTCTTTCAACACGGAAGTATATGAA
TGTCTGTAAGGAAACCACTGGCTTGATATTGATTTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACACCTCGTGAATAAGAGCTCCATTACAGAAAGTGGAACATAAGAGAAAGAAAGGGCAGA
ATATCAACACAGTGAAGGGAAGTATAGAGATGATTTTGAATGAACCTGTTTTTCTGTAGAC
TAGCTGAGAAATTTGTGACATATAAATAAGAAATGAAGAAACACATTTTACCATTTGTGAA
TTGTTCTGAACTTAAATGTCCACTAAAAACAATCTAGACTTCTGTTTGCTAAATCTGTTTCTT
TTTTCTAAATTTCTAAAAAAAAGAGGTTTACCTCCACAAATTGAAAAAAAAGAAAAA
AAAAA

FIGURE 20

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATGAAACCTCAAATTTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAAC TTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATT TTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCGCTTGCCTGCCGGGCCCGGGGAGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAGAATGTCGCGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGAG
CCGCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCAGAGCCCCGAGCGCATCCCGTTCGCCGCCAGCTCCCGCACCCCATCGCCGG
AGTCGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGTTCACGTATGG
ATCCTGGCCGGCTCTGGCTGGCCGTGGCCGGGGCCCCCTCGCTTCTCTGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTTGCGGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGC
CAGAGCGCGCACAGTTTGTCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACACGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCGCCCAGATGGCTACAAATGTGTACCGA
TCCGAGAAGCACCGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTTCGCCCTTGGAGACCGACAGCATG
GACCATTTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT
GAGACCATGCCGGGCTTCTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCTCTGAGTCCAGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCTGGGCCCCCATTTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTTCCCC
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTCTGAGAATAAATTGCTGTCTCCGGTGTCACTGCT
TTCATCTCCCCAGCCACAGCCCTCTGCCACCTCACATGCTCCCATGGATTGGGGCT
CCCAGGCCCCCACTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCATAAATTGCTGTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTTCCCGACACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTCTTACATTATTTATGCCCCCAATATATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAATAATGGAGTTTGTGTTG

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FIGURE 22

MRSGCVVHVHILAGLWLA VAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVLR T VAIKGVHVSRYLCMGADGKMQLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

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FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTTCTCCAGATTAGAGTGAAGAACTGGGTGCGAGTGCTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGTCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAACTGGAAC
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTTCTCATCTAA
AGCCACGACAATGAGTGAAAAATGTGAGTGGCTCACGCCTGTAATCCAGCAGCTTTGGAAGG
CCGCGCGGGCGGATCACGAGTCAAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLLED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRIGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTVPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

102120-2281050

FIGURE 25

GCACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
 AAAAGAAGAGGAAGATGTTGGGCAACATTATTATTAAACATGCTCCACAGCCCGGACCTGGGCAT
 CATGCTGCTATTCTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTTAAATAA
 ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
 TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGACAATG
 CAATTTGTGGCACTGGCACCTTATTTTCAGTGAAGAAAAAATTTGTGGTCTATGGCAATTCATCA
 TTTGCAAAATGCAAGCATCTTCTCTATCAATCAGCTCCTATTGAACTTACTAGCACTGACCTG
 TGGATCCTTAAAGGGCCCATACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
 CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCAGATCCATTTAT
 ATGGAAGCATCTACATGGATTGTAATGATTAGGTCTTTTAACTTTCCAGCCAGATTGCC
 AGCTAACACACAGATTCTTCTCTACAGACTAACAATATTGCAAAAATGAATACTCCACAG
 ACTTTCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTTCAGTCACCAAT
 ATTAATGTAAAAAAGATGCCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA
 ACTGCCGTAAAAATGTCTGTGCGAACTGAGCAACTTACAAGAACTCTATATTAAATCAACACT
 TGCCTTCTACAAATTTCCCTGGAGCCTTTATTGGCCTACATAAATCTTCTTCGACTTCATCTC
 AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGTATGCTCTTCCAATCTAGAGAT
 TCTGATGATTGGGGAAAAATCCAAATATACAGAATCAAAGACATGAACTTTAAGCCTCTTATCA
 ATCTTCGAGCCTGGTTATAGCTGGTATAAACTCACAGAAATACAGATAACGCCTTGGTT
 GGACTGGAACCTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAATCTCAAAATTTTGGATCTAAATAAAAAATCCTATTATAGAA
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAAATAATGCTCT
 GAGCTGATTTCCATCGATAGTCTTGTCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACCAACCTAGATTGTCTTACATTCACCCCAATGCAATTTTTCAGACTCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
 CCAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
 GATGAACATGAACAAAAACCAATTCGATTTCATGGAGCCAGATTCACTGTTTTGCGTGGACC
 CACCTGAATTTCAAGGTGAGAATGTTTCGGCAAGTGCAATTTAGGGACATGATGGAATTTGT
 CTCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAATGTAGAAGCTGGGAGCTATGT
 TTTCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTCTCG
 GTCAAAACTCTTGCTTAATACCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
 GATATAAATGGCGTAACCTCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
 GCTCTTTGAATATTAATAAAGAGATATTGAGCCAAATTCAGTTTGTGGTCTCTGGAAAGCA
 AGTTCTTAAATTTCTCAAATCTAGTGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAAATCTCA
 TGCTGCGCAAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
 CATCAACTGAGTATAAAATTTGTATTTGATATTCCACCATCTCAGAAAAACAGAAAAAAA
 TGTGTAATGTCAACCAAAAGGTTTGACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
 CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATGGTGTGATATGTCTTATCA
 GCTGCCTCTCTCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTTACTTACAG
 AAACCAACCTTTGCAATTAGGTGAGCTTTATCTCCTCTGTATAAATCTCTGGGAAGCAGGAAA
 AGAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTCT
AAAAACCCAGGAAACCTACTCCAAAAATGAAC

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FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVCPRCTCEIRPWFTPRSIYMEASTVDCNDLGLLLT
FPARLPANTQIILLQTNNTIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTPEKCLSELNLQELYINHNLSTISPGAFIGLHLLRLHLNSNRLQMINSKWFDA
LPNLIELMIGENPIIRIKDMNFKPLINLRSLVIAGINLITEIPDNALVGLENLESISFYDNRL
IKVPVHALQKVVNLKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGTIESLPNLKEISIHNPIRC
DCVIRWMNMNKTNIIRFMEPDSLFCVDPPEFQGGQNVVRQVHFRDMMBEICLPLIAPESFPSNLNV
EAGSVSVFHCRTAEQPEIYWIITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGFSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKTAFV
KTENSHAAQSARIPSDVKVYNLTHLPSTYEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLVKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

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FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCTTCCCCTCTCCATGTGCTCCTCCTACAAAGTTTGTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAACGTCCTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTTCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAGCAAATAAAAGCTTAACCTTGAAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLC SSSGGLNVTCSNANLKEIPRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTL DLSDN R
IQSVHKNAFN NLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNL PKKTTDYAMLVTMFGWFTMVISYV VVYVRQNQEDARRHLEYLKS LPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATG CAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGTCT
GGGCTCAGTGCTGT CAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTTCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAACCGCTCAACCAGGACGAGTTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTTCGCAGCAACCCCTGAAGTCTATC
CCGCTTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACC GCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAACT
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCCGCTCTGTGGGTGTTCCGG
CGCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCGCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACTGCGCCGCGG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACAGGTGCAAGTTT
GTGTGCCGGGCCGATGGCGACCCCGCCCGCCCATCTCTGGCTCTCACC CGAAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACCGGGCGGCAACGAC
TCCATGCCCGCCACCTGCACTGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTTCATCTCCAACAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCTTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCTGCTCCTCTCTTCGCTGGTGTGCTGCTTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACAAATCGAGATCGAGTATGTGCCCGAAAAGTCGACACGAGGCATCAGTCCCGCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGCGGGGGGAGGGGACCCCCG
GGCGCCGGGCGAGGGGAAGGGCCTGGTGCACCACCTGCTACTCTCCAGTCTTTCACCTTC
CTCCCTACCTTCTACACACGTTCTCTTTCTCCCTCCCGCCTCCGTCCCTGCTGCCCCCCG
CCAGCCCTCACCACCTGCCCTCTCTTCTACCAGACCTCAGAAGCCAGACCTGGGGACCCCA
CCTACACAGGGGCAATTGACAGACTGGAGTTGAAAGCCGACGAAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTGGGTTTCAATAATTATGGAATTT
TATGAAAACTTGAANAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCATCCCCAGCCCCCGGGATTCAAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTGCGCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGCTGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCACTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCTCTGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCTGAAGATGACCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCCTGCCCACTTCTCTGC
GCCCCCAGGGGCCCTGTGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC
CAAAACAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

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FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTRREDDGASIVCSVNHESLKGADRSTSQRIEVLVYPTAMIRPDPPHPREGQ
KLLHLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIIMLIFLGHYLRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTCTCCTTTCTGCTG
CTTCGGACATTGGAGCACTAAATGAACCTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTTGGATTCTGTT
GCTGGAGACGTCTCTTTTGTTTTTCGCGCTGGAAACGTTACAGGGGACGTTTGCAAGAGAAGA
TCTGTTCTCTGAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGGCTTCA
AGTCTGCAGCGTTTCACTGCCCGGACTTCCCAGTTTACCATTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATATGCGGTTAGTTTGCACATGG
AAAACAATGGCTTGCATGAATCGTTCCGGGGGCTTTTCTGGGCTGCAGCTGGTGAAGAAGG
CTGCACATCAACAACAACAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAAATTATACAGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAAACAGGCTGAAACCGTGCC
CTATGAGGAGGTCTTGGAGCAAACTCCCTGGTATTGGCGGAGATCTGCTAGAGGATAACCCCT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAAATGGCTGGAAAAACATTCCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGACAA
CACCGAACAGGAGCTTGTCTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGCGGCCCTTCG
CCCCAAGAAGAGACCTTTGCTCTGGAGCCCTGCCAATCTCTTCAAGACAATGGGCAAGAG
GATCATGCCACACAGGGTCTGCTCCAAACCGGAGGTACAAAGATCCAGGCACTGGCAGAT
CAAAATCAGACGCCACAGCAGCATAGCGACGGGTAGCTCCAGGAACAACCCCTTAGCTAA
GTTTACCCTGCGCTTGGGGGCTGCAGCTGCGACCACATCCAGGGTTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTCAGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTTCTGTGGATTCTGGGCAACAATAACATCGCTACTGTAGAGAACCAACCTTCCAG
AACCTTTTGGACCTCAGGTGCTATACATGGATAGCAATTAACCTGGACACGCTGTCTCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTCGGGGTCTCGCTCTTAAACTCAGCCTGCAAA
CAATTACTTACGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGAAACCCCTGGGAGTGCTCTGACAAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTTTATGCTCTCTCCAAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
GTTTGTCACTCCGCTTACCCTGTTGGGCTGCTCGTGTATTCTCTGAGGAACCGAAAGC
GGTCAAGAGAGCAGATGCCCAACTCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT
GACTCTTCTCATGGCACAATGGGCCTTACAACGCAGATGGGCCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGAAGCGG
ATACATCTCTCCCCACCGCAGGCCCCCGGGGCTGGAGGGCGGTGATCCCAAACTCCCGG
CCATCAGCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGACAACCGAAAGGGGCT
GACCCCTTACTTACTGCTCCCTCTTGAACAAGAGCAGACTGTGGAGAGTGGGAGAGCGCA
GCCAGCTCGCTCTTGTGAGAGCCCCCTTTGACAGAAAGCCAGCACGACCTGTCTGGAAG
AACTGACAGTGCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCGTGTATGGCTCCCTGTTGGCTACGCGAGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

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FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTQSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENGLHEIVPGAFLGLQVVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLVLILNDNLISTLPANVFQYVPI THLDLRG
NRLKTLPEYEEVLQIPGIAEILLEDNPDWCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHIPGSGLKMNCCNNRVSSLADLKP
KLSNVQELFLRDNKIHISIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNALQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCCTIVPFQWAERLGEVLSMDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTVVGMLVFILNRNKRKRKDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCCTGTACCCGGCGCCAGCTGTGTTCCTGACCCCAAGAATAAATCAGGGC
 TGCACCGGGCTGGCAGCGCTCCGCACACATTTCCTGTGCGGGCTTAAGGGAAACTGTTGGC
 CGCTGGGGCCCGGGGGGATTCCTGGCAGTTGGGGGTCCTCGGGAGCGAGGGCGGAGGG
 AAGGGAGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCCTCCAGACAC
 AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCTCAG
 AGAATGAGGCGCGGCTTCGCCCTTGCTCTCTGGCAGGCGCTCTGGCCCGGGCGGGCGG
 CGGCGAACACCCCACTGCGCAGCGTGTGCTGGCTGCTCGGCCCTCGGGGGCTGTACAGCCTTC
 ACCACGCTACCATGAAGCGGCGCGGCCGAGGAGGCTGCATCTCTGCGAGTGGGGCGCTC
 AGCACCGTGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTCTGCGGGCAGGGCCAGG
 GCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
 GCACCTGGAGAACGAGCCTTTGCGGGGTTCTCCTGGCTGTCTCGACCCCGCGGCTCTC
 GAAAGCGACACGCTGCAGTGGGTGGAGAGCCCCAACGCTCCTGCACCGCGGAGATGCGC
 GGTACTCCAGGCCACCGGTGGGGTCGAGCCCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
 GCGCAACCGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
 GCGCCTCTAAGTTGAGCTATCGCGGCCCTTCCAGCTGCACAGCGCGCTCTGGAAGCTCAG
 TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
 TCGCGGACGAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTGTGTCTCTGCC
 GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAAGCTGCTAGACGACTTGGGAGG
 CTTTGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGCGCCTCTGTGTGACCA
 GTGGGGAAGGACAGCGCAGCCTTGGGGGGACCGGGTGCCACACAGGCGCCCGCGGCACT
 GCAACGAGCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
 ACCACTTGTCTTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTCTGATGGGGAT
 CACAGAGCAGATGTCTACCTTCAAATGTCCCTTCAAGCCAGTCAAAGGCCACTATCACC
 CCATCAGGGAGCGTGATTTCCAAAGTTAATTCTACGACTTCTCTGCCACTCTCTCAGGCTTT
 CGACTCTCTCTGCGCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGTGATCT
 TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCTCTCTCCAGCCA
 AGGAAGGAGTCTATGGGCGCGCGGGCTGGAGAGTGATCCTGAGCCGCTGCTTTGGGGTC
 CAGTTCTGCACATTGCACAAACATGGGGTGAAGTCGGGGAAGTGTGATCTGCGGGACAGAG
 CAGAGGGTGCCCTGCTGGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
 CATGGGCACTCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACTTAC
 TTGTGTAAGTGAACATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG
 GAGCTAAATCAGAACTGCACACTCTTCCCTGATGATAGAGGAAGTGAAGTGCCTTTAGGA
 TGGTGATACTGGGGACCGGGTAGTGCTGGGAGAGATATTTCTTATGTTTATTCGGAGAA
 TTTGGAGAAGTGATTGAACTTTCAAGACATTGGAACAAATAGAACAAATATAATTTACA
 TTAATAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTTGTTCAAGCTAGGAGTAT
 ATTGGTTCAAATCCAGGGAAAAATAAAATAAAATAAAGGATTGTTGAT

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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIAD EIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPS SQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLDRDAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAAGTGCCTCCGCCCTGCGCGCCGCGTATC
CCCCGGCTACCTGGGGCCGCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGCGCGCGCGCCGTGGGGTGCAAACCCGAGCGTCTACGCTGCCATGA
GGGGCGGAAACGCCCTGGGGGCCACTCTGCCTGCTGTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCTCCAAATAGCAAATGTACTTGGAAAAATCA
CAGTTCGGAAGGAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAAAC
CCCCAACTGGCCAGACCGGGATTACCTTGCAGGAGTCACTTGTGTGTGGCAATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTTCAGGCCAAAA
AAACTGCCACAACTACAGAACAGCCTGTCAACACCAATTCCTGTAAACACGGGTTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CAGCCACAGTCTCGATCATCAACATCTACAAGAGGGAAATTTGGCGATTTCAGCAGGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCTCGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAACTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTC
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCCACTTACTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTATAGT
GTTATTTGTTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCCTTTTCTA
AATCAATGCTTAAATAAAATATTTTAAAGGAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTECGGILTGESGFIGSEGFPVPPNSKCTWK
ITVPEGKVVVLNFRFIDLES DNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSA AEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSEARNELLI
QFLSDLSLTAGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFCKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

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FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCGCGGGCTGGGGCGGTGCGTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCGCTCAGCCCCATCCGTGTATACCTG
CCGGGAGACTGGTTGACAGCTTTAACAAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCAAATACAAAGACAGTGAGACCCGCGCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCBCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGTGCCCCGCGAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTCTGGGGGAACAGAGAGGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCTGTGCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCATGCAAGAAGGG
CTGGGCCCTGCATACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCGTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACCTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGGAGAGTGGGGTAAGCACCCTTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGTGGATACCATGAGCTCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCTTAATGGTGGCTGTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGTGCATGCTGCCAGTTCCTGT
TCTGTGTTACACATCCCCACACCCATTGCCACTTATTATTATCATCTCAGGAAATAAAGA
AAGGCTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAA

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCGCGGGCTGGGGCGGTGCGTTCTT

09/07/2011

Signal sequence:

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Aspartic acid and asparagine hydroxylation site.

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCCCCTTGGACAGGGCCGACATGGAGGAGCTGGTATCCCCACCCACGTGAGGGCCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTTCAGCCAGAGC
TTCGAGAGGTGGCCGCGAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGCGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTTGCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCTTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTTGGCCTTCAAGTGGC
CGTTTCTGGGGCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTCTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCTACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCCANTGTGTCTATTGTTTACTTGTCTGTAC
TGGACTCTGGGCTAAAGTCTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAAATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPASPGGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRSLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLDGYGAQ
GDCDFEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCTTCGGCGGCTGTTGTGTCAGTGCCCTGATCGCGATG~~GGG~~GACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAASTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCTACGAATCCCAAAAGCACCCGTGCCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCCCTGTGAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTCTCATGCTGGCAGCCGTCCTTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCTTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTGGCTCACCGCTATCATCTGCATTGCGCTTACT
CAGGTGCTACCGACTCTGGCCCTGATGTCTGTAGTTTTCACAGGATGCCTTATTTGTCTTC
TACACCCCAAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTAAA
GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAG
GATTTAAAACCGTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCAGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTTACTGAAAATACAAAGTTAGCCAGGCATGGTGTGTCATGCCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLS CAYS GFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGT YTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLT CSEQDGSPSEYTWFKDGI VMPTNPKSTRAF SNS
SYVLNPTTGELVFDPLS ASDTGEYSCEARNGYGT PMTNSNAVRMEAVERNVGVIVA AVLVT LI
LLGILVFGIWFAYS RGHFDR TKKGTS SKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

030619Z JUL 74 071204Z

CACGCGCTGGCCGGGCGCCGCTGTGGGGACAGCATGAGCGCGCGGTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGCAGCCCGCTTTCCACCCCGACCTCTGCCACGGCCGCAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCAGTGCCGACCCAGTGGCCTTATGGGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCGAGCATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTATCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCAGTACTGCTATTCACCTCAGCTGGCGCTGCGACGCCA
CCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAAACCAATGAGATCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCTTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCTCT
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCAACGCCACCCTCTCTCTTTGTCTGGCTCCGAGCCAGGAGCGC
CTCGGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGTGCCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCGACACCAGCCCTCAGAGACCTGAGTTCCT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGGACTCTCCCTATGAGAGATCCGGGGAGCTAGAGTGGGGAACCTGCCACAGCCAGAACTGAG
GGGACTGCCCCCCAGGACGCTCCCAAGGGGTAGAACCGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGCTGGCGATTAAAGTTTGCTTC

07-00000000

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGGCGGCAGCAGAGGTCGCGCACAGATGCGG
 GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
 CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATATCATGGAATGAACCCGAGCAATG
 GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
 GCCGTGATCCTGTGGTTTACGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
 CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
 GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
 GGCCTACAAAGAGACTGTGTTTGAAGCATTTAATGGAACCCCTAGGCTGGATCCCAAGTGA
 TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
 ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG
 TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGACC
 CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
 TCCAGACCTCCTTCCCGGTGGGACTGTGATCTCCTATCGCTGCTTTCCCGATTAAACTT
 GATGGGTCTGCGTATCTTGAGTGCTTACAAACCTTATCTGGTCTGCTCCAGCCACCCCGGTG
 CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCT
 GCCACCCGCGCCTTGTGAGCGCTACAACCACGGAACGTGGTGAGTTTTACTGCGATCCT
 GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTTC
 TTATCAAGTCTACTGCATCAAATCAGAGCAAACTGGCCAGCACCCATGAGACCTCCTGA
 CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATC
 CTGGCCAGGATGTTCCAGACCAAGTTCAGAGCCCACTTTCCCCCAGGGGGCTCCCCGGAG
 TTCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG
 ACGAAGCTGTGAGTGGCGGCTTGAGTGCTTAGGCCCCGGGTACATGGCCTCTGTGGCCAG
 GGCTGCCCTTACCCTGGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
 CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGTCTCAAA
 GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAACCTGACATA
 ATTGCCAGCACGGCAGAGAGGTGGCATCCACGACCCAGGCATCCATCATGCCCACTGGGT
 GTTGTCTCTAAGAACTGATTTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
 ATACATGTGTGATCTGTGGAGTTGATTCCTTCTCTTGGTTTTAGACAAATGTAAACAA
 AGCTCTGATCCTTAAATGCTATGCTGATAGAGTGGTGAAGGCTGGAAGCTTGATCAAGTC
 CTGTTTCTTCTGACACAGACTGATTAAAAATTAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFLQALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLVLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQCPLPVDDQSPPAYPGSGD TDTPGGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGDWFWIGLRREEKQSNSTACQDL
YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLV
VTTVVCWWVICRKRREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCCGCTGAGCCCCGGCGCCCCGAGAAGACTTGT
GTTTGCCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACCTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAAATGGTGCAAGTCTGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCAAGCTATTAGAGGTCCCAACCCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCCACTGATGAAGCAGATTGAGAAGTCTGTATCCCACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCAAGTTTATACCTTAAGCCCAGAAAAATACCATGCATCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCCTTTATACAATG

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FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRVALAELQEADGQCPVDRSLLKLMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFRARMIEQRAVDTSLYILPKEDRESLQMAVGPFLLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGGCGCTGTTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCCTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGTGTGAGGTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGGCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCATCTGGCTGAGCCAGATGTGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTTCTGGGCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGCTATGCAAGCAACTGGGCTGTGGGAAGTCCCCTCTCTCCCTCCTTACAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTACAGATTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACATACATCA
CCACCTTTCTTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTTATTTACAATAATAAGATAGCAC
TATGTGTTCAAA

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FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCSEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGC GAASGTPSGILYEPPEAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSFSFPVPEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSSCGREATLQDCPSGPGWKNTCNHDEDTWVECEDPPDLRLVG
GDNLCSGRLEVLHKGWVGSVCDDNWGEKEDQVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNRVCSGEEQSLEQCQHRFWGFHDC THQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

0900497-07201
102720-280650

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCGCTGCTGTTGCGGCTGCCTGGG
CGTCTTCGGCTCTTCCGGCTGCTGCAGTGGGTGCGCGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGCTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACC GCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCTTCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGACGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTAAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTAC

09004877-071201

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAABEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAACCGCTCGCAGCCACAAAAGGGAATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCCTTACTGATCGTCTGCTCCCTAGAGTCCCTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAAATCAGTACC CGCGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAGAAGGTGAAGGCAGAAATG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAA
GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTGGGA
TTTCATAAAACTTTGACAGATGAAGTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTATTCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATTAAGCACCTAGTTTTCTGAAAACGATTTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTGAACCTCTGTTTTTCTAATTATCCCCATTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAATGACTTTATTTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTGTACCATAACCGTTTATTTAACATATATTTTATTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACCTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCTCTGAGAGATACCTCACATTTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

09904877-071504

FIGURE 58

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAETGDSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHI VTVASAAGHVSV PFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMFIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
AGGGAGGAGCACCAGACTGCGCCGACCCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTGGGCCCTTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCAGCTCAGATACAGC CAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGTTGGGCGGG
ACGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGSCCTTATGTTGTCAAGTAACATGA
CCTTTCGGTGACAGAGACTTCCCTGGACCAACAGCTCTCCATGCTTTACATTGCACAAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACATAATTCAGTTTTTCCAGATATTTCTTGAATATAAAAAATA
ATGACTTTTATGTCACTGGGAGTCTTATGCAGGGAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTTGGCT
TGTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACAATC
AGGAAGCAGAAGTGGTTTGGGCCCTTTGAAATACTGGATAAATCTAGATGGCGCACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTTACTATAAATTTTTCGGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGAG
AGATACAGTACAGTCACTTAAGCCATGGTTAACTGAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACCTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAAGGATCCAGGAATA CAAGAAGGCAGAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAAATTATTC
GAGGTGGAGCATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAGAGGATGGGATCCTTATGTTGGATTAACACTACCTTCCCAAAAGAGAACAT
CAGAGGTTTTTCATGTGAAAAGAAAATCGTAAAAACAGAAAATGTCTAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTAGGCTCTTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAGTGAAGTGACGTTG
TAACAAACAAAGCTGTAAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAATAAATGGATGAAGCTATAA
TAGTTTTGGGAAAAGATTCTCAAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAAATATTATATAAAAGTAAAAA

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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPPFGLNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWT'TTLSMLYIDNPGVTGFSFTDDTHGYAVNEDDVARDLYSALIQT
FQIFPEYKNDFYVTGESYAGKYVPAIAHLIHS LN PVREV KINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVGTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR EDTVQSVKPWLT
EIMNMYKVL IYNGQLDIIVAALTERSLMGMDWKGSQEYKKA EKKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWD PYPVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

102120-230000

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
TTTTCCCTTTCTTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCTGCCATAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAAATAAAATTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAAGTATGTTAAAAATA
GAAAAACCAAATGCGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGAAATTTATTTTGGTCTGACCACTCTGCCTTGTTTTT
GCAGAATCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCGCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAAATCGTGACTGGACCTTCAACCCTTGACCGT
CCACCAAGGGACGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCCCTCACCACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGCTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCAACAAGAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTGCCA
GCCGAAGCTGCCCGAGACCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTTCAGACACCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGTCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCTGTCCG
CTCTCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCTGCAAGGTGCTTACCTGGCCAAGCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTGCCATCTTCCAAAGGGCAGAAG
CAGTATCACCAACCCCGCATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACT
GCAGATCAAGGAGCGCTGCACTCTGCTACCAAGGCGGAGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
CAGCAGGACCCGATGACCTCTGTGGCCTCCTACGTTTACAAACGCTACAGCGTGGTTTGTG
TGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAAGAGTCTATGAGTTCAAGTGTCCCAATGCC
ATTACCTCTCAGCAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGTGAATGGGAGGTAAAGAGGGGTTAATTTTGTG
ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCACTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTAAGAAAAAAGCTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 62

MGTLGQASLFAPPGNYFWSDSHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEDDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFLVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPRESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFGGFFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAAQFNITSQDDVLFAlFAFSKGQKQYHHPDDSalCAFPiRAInLQIKERLQSCYQGEgN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRTSVASyVYNG
YSVVFVGTKSGKLKKVRVYEFRCsNAIHLLSKESLLEGSyWWRfNYRQLYfLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCCGCGCGGCTGAGTGGCGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAAACACGCGATGACCA
 CGTGGAGCCTCCGCGGGAGGCCGCGCCGACGCTGGGACTCCTGCTGCTGGTGTCTTAGGGCTTCTGGTGTCTCC
 GCAGGCTGGACTGGAGCACCTTGGTCCCTTCGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
 ACTTTCATCTGGAGGATCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCGGTGTGCCAGGGAGTACT
 GGAGGGACCGCTGCTGGAAGATGAAGCCCTGTGGCTTGAACACCCCTCACCACTATGTTCCGTGGAACTTGCATG
 AGCCAGAAGAGGCGAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGCTCTGATGGGCCACAGAGATCG
 GGCTGTGGTGATTCTGCTGCTCAGGCCCTACATCTGCAGTGAGATGGACCTGGGGGCTTGGCCAGCTGGCTAC
 TCCAGAGCCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCAACCAAGCAGTGGACCTTTATTTTACACACC
 TGATGTCTCAGGGTGGTGGCACTTCAGTACAAGCGTGGGGGACCTATCATTCGCGCTCAGGGTGGAGAAATGAATATG
 GTTCTATAATTAAGACCCCGCATACATGCCCTACGTCAGAAGGCACTGGAGGACCGTGGCATTTGTGAACCTGCT
 TCCCTGACTTCAGACAACAGGATGCGCTGAGCAAGGGGATTGTCCAGGGATTTGGCCACCATTCAACTTCAGT
 CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGCTCCAGGGGACTCAGGCCAAGATGGTGTATGGAGT
 ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCTCACAAATATCTTGGATTCTTCTGAGGTTTGAACACCGTGT
 CTGCCATTGTGGACGCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCCAACCTTTGGCTTTCATGAATG
 GAGCCATGCATCTCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
 ATTAACAGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCACTCCCTCTCCCTCCCCACCTG
 ACCTTCTTCCCAGATGCGGTATGAGCCCTTAACGCCAGCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
 TGGGGAGCCAACTCAAGTCTGAAGAAGCCATCAACATGGAGAACCCTGCAGTCAATGGGGAAATGGAGCACTGCT
 TCGGGTACATTCTCTATGAGACCAGCATCACTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
 TGTTTGTGAACACAGTATCCATAGGATTTCTGGACTACAAGACAACGAAGATGCTGCTCCCTGATCGAGGTT
 ACACCGTCTGAGGATCTTGGTGAGAATCGTGGCGAGTCAACTATGGGAGAAATATTGATGACACGCGCAAG
 CCTTAATTGGAATCTCTATCTGAATGATTCAACCTTGAAGAACTTCAAGATCTATAGCTTGGATATGAAGAAGA
 GCTTCTTTCAGAGGCTCGGCTCGGACAAATGGNGTCCCTCCCGAGAAACACCCACATTAACCTGCTTCTCTCTGG
 GTAGCTTTGCTATCGACTCAACGCTTGTGACACTTTCTGAAGCTGGAGGGCTGGGAGAGGGGTGTATTCA
 TCAATGGCCAGAACCTTGGACGTTACTTGGAACTTGGACCCAGAAAGCGCTTAACTCCAGGTCCTCTGGTTGA
 GCAGCGCATCAACCAAGTCTCGTTTTTGAAGAGAGATGGCGGGCTGCATTACAGTTACCGGAAACCTCCAGG
 ACCTGGGCGAGAACCACTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGTGTGCTGAGGAGAGCTGCGCCCT
 CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCAACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG
 ACTGGGGCTCAGCTCTGCCCTGTCTCAGCTCAAAACCTTAAGCCTCGAGGGAAAGGTGGGATGGCTCTGGGG
 TGGCTTTGTGTATGATGGCTTCTTACAGCCCTGCTCTTGTGCCGAGGCTGTGGGCTGTCTCTAGGTTGGGAGC
 AGCTAATCAGATCGCCCAACCTTTGGCCCTCAGAAAAGTGTGAAGCGTGCCTTGCACCGGACGCTCACAGCCC
 TGCAGCATCTGTGACTCAGGCCTGCTTCTTGTGGTCTTGGGAGGCTTGGCCACATCCCTCATGGCCCAT
 TTTATCCCCGAAATCTGGGTGTGTCAACAGTGTAGAGGCTGGGGAAGGGGTGTCTCACTTGAGCTGACTTTGTT
 CTTCCTTCAACAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACCTCGGCTGAGAAACATGTGACTTCCCTT
 TCCCTTCCACTCGCTGCTTCCACAGGGTGAACAGGCTGGGCTGGAGAAACAGAAATCTCACTCTGCTCTTCC
 CAAGTTAGCAGGTGTCTCTGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
 CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCC
 AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCCAGGGAGGAG
 ACAGAAGGCCACGCTCAGTGGCCCCGCTCCCAACCCCAAGCCGCAACAGCAGGAGGAGGAGGAGGAGGAGGAGG
 GAAGTGTGTCCAAGTCCGACTTTGAGCCTTGTCTGGGGCCAGGCCAACCTGGCTTGGGCTCACTGTCTCTGA
 GTTGCACTAAGACTATAACCTTGAATCAAA

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGGTGAGGGTTCTCTACTTGGCCCTTCGGTGGGGGTCAAGACGCGAGGCCACTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGGCTCCC
 AAGAAGCTGTCTGCCTTCGTTCCTGCTGTGTCGCCGTGACGCTGACGCTACTGTCTGCCCCA
 GGCAGACACTCGGTCTGTTCTAGTGGATAGGGGTGATGACCGGTTTCTCCTAGACGGGGGCC
 CGTTCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACATA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTATTGGCTTTTGTGA
 ATGAGGCAGCTCTAGCGAACCTGTTGGTTCATCTAGAGACGAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCCTC
 AGATCCAGACTTCCTTGC CGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTTCAGGTGGAGAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCGGTGCACGTGCTAGG
 AGAAAAGATCTTGCTCTTCACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTCTATACCACTGTAGATTTTGCCCGAGCTGACAACATGACCAAAATCTTTACCCTGGCTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTAT
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTCAACACTTTGGATATTGG
 AATGTTGCCGATAAGAAGGGACGCTTCCTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGTCTCTCGAGATGTATCAGCAAGT
 TCCAGGAAGTTCTTTGGGACCTTTACCTCCCCGAGCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT
 TCATCTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGTTCTATGTTGTAC
 GAACCTATATGACCCATACCATTTTTTGTAGCCAAACACCATTCGGGTGCCAAATAATGGAGTC
 CATGACCGTGCCATGTGATGGTGGATGGGGTGTCCAGGGTGTGTGGAGCGAAATATGAG
 AGACAAACTATTTTTGACGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCTCTGTTGAAGCCACCAATTCG
 GGGCAAAACAATCCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
 GTGGTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAAACATTTTCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGCCGGTACTGGACAAAGCAGGGGCC
 ACAACAGACCCTCTACGTGCCAAGATTCTGCTGTTTCTTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAAC TAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC
 CTCGAATGACACTAGTACTTTGCA CAGGACACATATCAATTCCTTTTCAGCTGATACACTGAG
 TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
 CTGTAAATCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGACTTCAAGA
 CCAGCTTGGCCAACTAGGTGAAACCCCGTCTCCACTAAAAATACAAAATAGCCGGGCGTG
 ATGTTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAAATGCTTGAATCC
 AGGAGGCAGAGGTTGCAGTGGATGGAGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
 GACACTCCATCTCAAAAAAAAAA

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FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRHDFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGPLSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGGLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFVWVN
NGVHDRAYVMVDGVFQGVVERNMMDKFLTGKLGSKLDILVENMGRLSFGSNSDDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDFTFLYL
PGWTKGQVWINGFNLGRYWTQKGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTLHRTHINSLSADTLASPEMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCCTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTGAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTGAGAAGTTAGTGAAAAATAAAGTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGTCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCATGCGCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCCTTACCGTGAAGTTCACTGATGTGGCTGAAATTCCTGCGTGGGTGATTTGTCTAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCTAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
GACTTGTTTTAAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACTTGAGTCACTTTATTTCTCTAACACAAGCTCGAATCCTTACAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATCCAAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATCTCTGC
CAAAACAATTGTTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAGTG
CTTGACCGCCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTTTGCAAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCAGGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTCTTTTGGGG
AAAGGAAGGAAAAATTATAATCACTAATCTTGGTCTTTTTAAATGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTAAAGTAAATGATTAAATTGACATT
TTCCTTACTAAAAAAAAAAAAAAAAA

[illegible]

CCACGCGTCTCGGCCCTTCTCTCGGACTTTGCATCTTCCTCTCTTTTCATTGACCAAACTGACTTTTATTTATTTCT
CTTTGTTTCATCTCTGCGCCAGCTTGGGACTCTAGGCCCGCTGGGGAAGCAATTGTGTTTTCACACATAGAGAT
CTGTGTTTGGGGTTTCTTCTCTCTCCCTTCACATTCGGCATCTGCTTAGTGGTTGTGTGGGGGGGAGACACAGCTGG
GCTCAGTGCTCTGCTCTGACTTATCTGCGCTAGGATCATCGAAGTCTTTTGACTCTTCATACGATTAATTGCTGCTGTC
ATCGCTGTGGTGTATCTGCTGCGGCTCTGTCTCTGTCTGATAGTTTGTGCTGTCTGTCTTCTCTCAAAATACACAA
GCCTCAAAAGCTCAAAAGGAACCTGAGCTGTGGCTGTGAAAAATCAZACCCGACAAAGTGTGGTGGGCGCAAG
AACAGCCGAGCCGCAAAATCTGCAACCGAGGATCTTTGTCTCGCCTGCGATGCTGTGAAGATATAGAATTGTGTGCC
AGTTTGGATCTCTGCCCATCTCTGCTGTGGCATATAAATGGGGCTCTGATGTGAGGAAGGCTCCCTTCTCAAA
CGAGAGCGCTTGAGATCTCAATGATTCGTAATGAGGCCATCTTTGTTGTGATGTGTGAGGCACAGAAAGAGGCGACAG
CTCCCCATCGATTTCATGAAAGAAATCATCGATGCTGCTGGGAACACAGCTCTGGGAGATCCCTACAGAGAGCTTC
CATCTGGGGGCAACCCCTTCAGGAAGGAGTTGGGAGGAGAGAACCTCATCTGCGGAAAGTCTGTGATAAACCAGTCA
CGATGTGCTCTATTTCACACAAATCTACCCTTTCGCTGTGGCTGGGAATGACGTTTCCCTGGAGGTTGTCAGAA
CAGCATGACACACAGAGCTATAAAGCTGTGGCTGTCTTAAGGCTGCCAGCGCCTGTGCGAAATGGAGCTTGTA
AGAGAGGCTCAGTCCATTGACCTCTTAATTCTCTCTCTCTTTGGCGGAGGCTGACATGTGGCGGAGGCTGGAAGCAAT
CGAAGCTGCACATGCTCAGTCTAGGGGGTGCCAAATATGGCAGAGACCAAGAAGCATGATCTCGCAATCAGATCCC
GATTGAGAACTGCACCTGGCAATAGAGAAGACCAAGAAACAAAGAGCATCAGAATATTCTTTCTCTATGTCTCAGCTT
GATTCAGATGTGAGGCTGTGAAAGTGAAAACTATAAAGTCTTTGACGGAACTTCAGACAATGGGCGCTCTGTGAGGG
CAAGTCTCGAGTAAAAACAGACTGTTCTGTGATTGTAATCATCTCCAGTACATGACGTTTCAAAATGAGTTACT
GACTCAGCAAGAACTCAAGAACTGTCTTTGTCTCTACTACTCTTCTCTCTCTAACTCATCTTATCTCAAACTGT
GGCGGTTGCTGGTATATCTTGAAGAGATCCTTCCACAGGCCCAATACCCAAAGCGCGCATCTGCTGAGCTGGCTCAT
TGTGTGTGGCCATACAGAGTGGGAGAGAAATACACAGCAATAAACTTAAACTCTAAAGAGATTTCTCTAGAAATAGAC
AACACAGTGCAAATTTGATTTTCTTCTGCATCTATGATGGCCCGCTCCACAACTCTGTGGCTGATTGGACAGACTGT
GGCGCTGTGACTCCACCTTCGAATCTGCAATCTCAATCTCTGACTCTCTGACTGTGTGTGTCTACAGATTTCGAATCT
TACCGGGGATTTCTGCTCTCTTACACATCAATTTAGGACAAAACATCAACATACATCTTTAACTTGTCTCTCT
GACGAGTGTGAGAGTTATTAATAAGCAAAATCTACCTTAGAGGCTTTTAACTCTAAATGGGAATAACTTGCAACTAAAA
GACCCAACTTCGACAGCAAAATTTCAAATGTGTGTGGAATTTTCTGCTCCCTCTAAATGGATGTGGTATCAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACCAAAATTAATCACTTTTCTGATCTCAAACTCTGAAGATGATCAGG
CGTCTGAAAACCACTCTCAGATTGTGTGAAGTGTGAAATGGGACATAATCTACAGTGGAGATATATACATACCA
GAGATGTAGTAAATACAGAGTCAAAATGCACTGGGCAATAAACACAGCATGGCTCTTTTGAAGTCAACTTCA
TTTGAAGAGACTATCTTAATACACATATATCTGTGGAATTTGAACAAACTCTTTTGTTCAGATTAGTCTGTGAC
AATTCAGCTCAAAATTTGGTGTGTTTCTTGATATGCTTAGAGCTCTCCACCTCTGACCTTTGACATCTCAACCT
TAGCATCTAATCAAGAGTGGATGTAGTCTGAGATGAACTGTGAAGGTGTATCCCTTATTTGGACATCTGGGAGA
TTCAGTTTAAATGCTTTAAATTTCTGAGAGATGAGGCTCTGTGATCTCGAGTGTAAAGTTTGTATGTGTGAT
AGCAGTGACCAACAGCTCTCGCTGCAATCAGGTTTGTGTCTCCAGAGCAAAAGACATCTTCTTATATAAATGG
AAACAGATCTTCATCTATAGGACCACTTCTGTGAAAGGAGTGAAGTGTGAGGCGCAATTCAGGATTTCAAGAT
GAAACAGCTCGGGAAGAAATCCAAACACGCTCTTCAACAGTGTGATCTGTCTTCTCATGTGTTCTAGGCTCTG
AATGTGGTGACTGTAGCGCAATCAGATGGAGCATTTTGTAAATCAAGGGGACATCAAAATACAGAGCTCTG
CGACATCATTTAACTCAACAGGTCCAACTTAAGTGAGACATGTTTCTCCAGATGTCCAAAGGGAGGCTCTACTCGT
GAGTACATATTTTATGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCGCTGATGTGAAATAAAA

FIGURE 70

MELVRLMLPLTLILLISCLAEITMAEAGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIIRIIFSYVQLDDPGSCSENIKVFDGTSSNGPLLGGVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFYFSPNISIPNCGGYLDTLEGSTSPNYPKPHPELAYCVWHIQV
EKDKYIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVPTPFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCCSSDRMRVIIKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGNST
VEIIYITEDDDVIQSONALGKYNTSMALFESNSFEKITLESPYYVDLNLQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDPASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAPKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGTC
TGCTGCCGCCGCCGCGTGCCTTGCCACAGCGCCACGCGGTTCCAGCCCACTGGGAGTCC
CTGGACGCCGCCAGCTGCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGT'TTCCGTGCCAGCTTCGGTAGCGAGTGGTTCCTGGTGGTAT'TGGCAAAAGGAAA
AGATACCGAAGTATGTGGAAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTAAATGCCAACCACTGAGGCGAGATATTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATAATTCGTGGAAC'TGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGT'TTGGAAGTGTACTATTCCCTTTTGA
ATGGTTTCATCCGCTCTTCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGCAGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAAC'TGCATGACAATAGACAAAAC'TGCTTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAA'TTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACTAGATGGCACCAATTCGTAGT'TTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTTGGCTAAAAGTCAATGGAGAAGCTATTTTGAACCTTA
TACCTGGCGATCCCAAGAATGACACTGTACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATT'TTCTTAAATGGCCACATCAGGACAGCTGTTCCTTGGCCAT
CCCCAAGCTATTCTGGGGGCCAACAGAGGTGAAACTACTGGGCCATGGACAGCCAATTAACTG
GATTTCTTTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAAATTA'TTGGCAGTTCAGCCCTTCCCTTTTCCCACTA
AATTTTCTTAAATTACCCATGTAAACCATTTTAACTCTCCAGTGCACTTTGGCATTAAAGTC
TCTTCACATTGATTTGT'TTCCATGTGTGACTCAGAGGTGAGAATTTTTCACATTATAGTAG
CAAGGAAT'TGGTGGTATTATGGACCGAACTGAAAATTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTGTGCCACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAAATACTGAAAATAAATGGTGCACCTGTATAGGGCACTTACCAGAAATGGAG
CTTACAGGACTGGAAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTTAGGACATTA
TTGAACACTGCCAGACGTTATAAACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTTCTTTCTTCAATATAAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTAAT
TTTAAACCTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACTCATTGTGCA
ATGTAA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPWTESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEFW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVGRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVPDWWYTSKPKEKLVAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

102170.4480660

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAAGTGTGAGCCTCAACATAGT
TCCAGAATCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGCGCCAGTGTCTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGACT
TTCATCCAGGTGTATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTACAGAAGCTAAGGAGGCTTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTGCTGGTCACTCTAGGATTAGCCAAACCCAAAGTGGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCATTCAGAAATTATCACCACCAAGATCCCATATTCAACACTCA
AACTGCAACACAAACACAGAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCTT
ACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTTGTGTACAGAAAGTTTATGGAAGTACGACCATGTCTACAGAAAC
TGAAACCATTTGTGAAAAATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTC
CCACGGCTCTGCTAGTGTCTGCTCCTCTTCTTGGTGCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAAATCAGCAGAAGAAATGAT
CGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAAAACCAGAAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGTCTGGAA
CTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCCCTGCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAAAGAAAGTCCACCCTT
GGTTCCTAACCTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGC
CCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTCTACCTCAAAGCTTCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCCGAGCTCAGAC
CCTTCTCTCAGCTCTGAAAGAGAAACAGTATCCACCTGACATGTCTTCTGAGCCCGGTA
AGAGCAAAAGAAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGTAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCCTGCTGATATTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAGTAATAAAATTA
ACAAACATTTGCTGAATAGTACTATATGTCAAGTGTCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTCAT
GTTTTGATATTTCTAGCTTATTCTACTTCCAACATAATTTTATTTTGTCTGAGACTAATCTT
ATTCAATTTCTCTAATATGCAACACTTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTTGTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTCCCAACAAGAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAAACTT

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FIGURE 74

MARCFSLVLLLTISIWTTTRLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPTNKNQQKEMIETKVVKEEKANDSNPNNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGCTCTTGGCACCTCTAATTGCTCTCGTGTATTCCGTGCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTCTACTCGTGAGGAA
ACTGCCGCGCTCTGCCACGGTCTGCCCCACCCAAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAAACAAAT
TCTTTTCTTCCGCTTGATATTCGCATGGGCCCTACTTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAAACGGGACAAGAGGTCACCTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCTGATCCTGTTCAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
CTNGACTGGNTGGGCGAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCTACAGGAAGGCCTGCCATGCTGTGGCCAACGTCTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGTTTCCCTCCAAGCTTGGGTCACTGTGTTAACTGCTTATC
AGCTATTACAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCACTATTCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTTCCCCAAGGACTCTTGCTTCTTAAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCTAAGGAGAAACCTTTAAACCAAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGAGGAGGAAATCCCTGGACTTTCAC
TAACCTCTGACATACTCCCAACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
TCCTTTTG

Abstract

Signal sequence:

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCCTGGCCCGGTACCCCTGGCATGAGGAGATGGGCCCTGTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGCTCCTACGGA CTGCCCTTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTG
CGTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCA TTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCCTGGGAGGAGGCGCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTG CAGTACCCCATCATGTTGCCCCGCGCAGCCCTGCGGTGGCC
CAGGCTGGCACCTGGCGTGCGAAGCTACGGCCCCGCCACCGCCCTGCACCGCTATGAT
GTATCTGCTTCGCTACTGCCCTCAAGGGCGGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGCAGAGGCAAGGGAGGCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
AGCTCTTTGCCGCTGGAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCCGACCCG CAGAGCCGCTTGTACGGTGT TACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT
CGTTTTCCCTTGTGGGTTGGAGCCATTTTAAC TGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTACTATTTTTTTGTAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCTGGGCCATTTGCGGTTTTTG TGGGCTTCTG
GAGGGTTCGCCGCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCCT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGCCCTCCGAGCTGGGCTTTGGGCCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCTCCCGTTCCCTT
TCCCTCTCGGTTCCAAAGAATCTGTTTTGTTGTCA TTTGTTTCTCCTGTTTCCCTGTGTGG
GGAGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGCTATGACTGCCTTCCGCCAA
AA
AA

0904077.071201

0987

Signal sequence:

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

LETTER

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGCTTCTGTGTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCAGACGCGAGGCCCTCATGSCCAGGGGAGGGTGCACAGGCGGGCCCCCTGAGCGACGCTCCCATGATGACGCCACGGGAACTTCACGATACGACCATGAGGCTTTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCACCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGACGGCGACGGCTGGTGTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCGAGCAGCGGCACTACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGACGGCGTGTGGTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCCGTGAAGAAATTCATGACGTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGCGTTCCTGGGTGGCGACCGGATGGGACCTCGATGGCCACTCGAGAGGACGACAGCCCTTCCTGCACCCCAGGAGTTCCTTCACTGCGGACATCGTGAATGCTGAAACCTTGAGGACCTGGAACAGAAAATGATGCTATGCTCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCGAGCCTGGGGAGGAGGAGCCGCGTGGGTGCAGACGGAGAGGCAGCAGTTCGGGACTTCGGGATCTGAACAAGGATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAGCCCCTGGTGGAAGCCAACCCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAAAGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGGACCTGACCCGSCACACGATGAGCTGTGAGCACCGCGCACTGCCACAGCCTCAGAGGCCGCACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCTGTCCAGGCCCGCAGGAGGCAGATGCAGTCCAGGCATCTCTCGCCCCCTGGGCTCTCAGGGACCCCCCTGGGTGCGCTTCGTCCCTGTCCACACCCCCAACCCAGGGAGGGGCTGTCTATGTCACAGAGGATAAGCAATACCTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTTGCCCCAAGCTCAGCTCTAAGAACCGCCCAACCCCTCCAGCTCCAATCTGAGCCTCCACCACATAGACTGAAACTCCCTGAGCCCCAGCCCTCTCTCGCTGGCCTGGCCTGGGACACCTCTCTCTGCCAGGAGGCAATAAAGCCAGCGCCGGGACCTTGAAA

FIGURE 80

MMWRPVSLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKFQDLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSDMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHWLPPAQDQPLVEANHLLHESDTEKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

0904577-071204
102720 225400

FIGURE 81

GGGGCTTGCCTTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
 GCGGCGGGCGCGGGTGCAGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCCGAG
 CCTGTCTGTCTGCTGCTTTTGGCGCCCCCGCTCCCGGGTGCAGACCCGATCCTG
 GGCTTCGCTCGATTTGGCGCCGAGGCGCTCCCGACCTAGAGGGGCGCTGGCCTGGAGCAG
 CGGGTCTGTCTGTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCAGGGGCTCT
 GAGGAGGTGACGCGCGGGGCTCCCGCACCTGGCCCTTGGCCCTTCCCGCATCTCCCTCTCTCCAG
 GTGTGAGCAGCCTATCAGTCACCAATGTCCGACGCTGGATCCCGCTCTCGGCCTCGGTGTG
 TGTCTGCTGCTGCTGCCGGGGCCCGCGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATG
 TTTTACCAGAGCTTTGGACATCAGGAAGAGAGAAAGCAGATGTCTCTGCCACGGGGGCTGCC
 CTCTTGAGGAATCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
 TGGTCGAGAAAATCTTCTCAGTAGATGCCAATGGCATCCAGTCTCAATGCTTTCTAGAT
 GGTCTGCTTCTTTACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
 GTGTCACAGCACATCCACCAACAGGTAACGACTAAAGAAAACCCCGAGAAGAAAAGTGG
 CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
 GCCGATTTAATTTACAGAAGAATTTGTTGGAAAAGTGGCTCTAATGTTGGGAATTTGGAACA
 GAAGGCCACATGTGGGCCCTTGTTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
 AAACCTTTACATCAGCCAAAGATGTTTGTGTTGCCATAAAGGAAGTAGGTTTACAGAGGGGTA
 ATTTCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATCTTCCAGGTAGATGCTGGA
 GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
 CGAGGAAGCAGGCATTTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
 AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTACATTTTGTGACAAGGCTGTCTGT
 CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
 GCCTCTGTACAGAAGCTGTGCATCATGAACAAATGATGTGCAGCAAGACATGCTATAACT
 CAGTGAACATTGGCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCCTC
 ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGACATTTGGTGCCAAGAT
 AGCTGCTGTACAGTTTACTTTATGATCAGCGCACGGAGTTTCAGTTTCACTGACTATAGCACCA
 AAGAGAATGCTCCTAGCTGTGCATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
 GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAAGAA
 CTTCTTAGTAATTTGTACAGATGGGCAGTCTTATGATGATGTCCAAGGCCCTGCAGCTGCTG
 CACATGATGCAGGAATCACTATCTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTTACAGGATT
 AGAACCAATTGTTTCTGATGTCTATCAGAGGCATTGTAGAGATTTCTTAGAATCCCAGCAAT
AATGTTAACTTTTGACAACGTAAAGAAAAGTACAAGGGGATCCAGTGTGTAAATTTGTATT
 CTCATAATACTGAAATGCCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGATATGTCAAC
 AGCCATTTAGGCAAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAACTCAGGAAAGAGGA
 GATAATGTGGATTAAACCTTAAGATTCTAACCATGCCTACTAAATGTACAGATATGCAAA
 TTCCATAGCTCAATAAAGAATCTGATACCTAGACCAAAAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEADVLCPGGCPLLEFSVY
GNIVYASVSSICGA AVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSQTQ EATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVLVQASEHPKIEFYLNFTSAKDVLF A I KEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVT FVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLC THEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRES PNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCC
GGCGGCTCCCGCGCGGAGCGAGCAGATCCAGTCCGCGCCGCGAGCGCAACTCGGTCCAGTCG
GGCGCGCGCTCGCGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCCTGC
TGTGTGGCGCGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCCGGCCCCGCTCTCAGTACCCCGCAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAACGTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT
CACAAATGAGACCAACACAGACACGAAGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCGACAAATGGGACCATCTGTGACAACAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCTGCTGTTCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCAGCCTG
GTGTATGTGTGCACCCGACCTCTGTGGGAGCCGTGACCAAGATGGGGAGATCTTGTCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGCGCTGGGGGAGCCTGCGGCTGCCCGCTG
GCACTGCTGGGAGGGGAGGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCAAGGTGTGTCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTACA
TCTTCTTCCCACTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCAAGTCTGGTGTGGGAGAGTCAGGAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGGGGAGGAGATGGAAAACATGTGG
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCTTGCTTTGCAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGAGTTCTTCCATGGGCATAGGTAAAGCTG
TGCCCTCAGCTGTTGCAGATGAATGTTCTGTTCACCTGCATTACATGTGTTTATTTCATCC
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCCAGCCTTGGTGCCACCA
AAGTGTCTCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACATAATCTCACATCCCTCTAAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGCTCTCTAATGAAGACAATGATATTGACACTGCTCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACCTGGAGAAAATCAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTAGGTGTCA
TGGACTGTTGCCACCATTGATTATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTCTTTGAGTTTAAATTTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

09904877.071201

[illegible]

Signal sequence:

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

03048747

AAGGAGGCTGGGAGGAAGAAGGTAAGAAAGTTAGAGAACTTCACTTCACATCTCTTGGGCTCAGAAGGACTCTC
AAGATAACAATAATTTACGCCATTCATCTCTCTCTCCCTCCAAACACACATGTGCTATGACACACATCATCA
CACACATACCTTCTCTCTCTCTCTAGTAAGCATCAGTCATCACTCTGTGAGCAGGTCTAGAAAAGGACAC
TAAGAGCTTTAAGGACAGGCTGGCCATTAATCTTGCAGCTCTCTTGGCTGTGTGAGTCAAAAACATCTGGAGGGG
CAGGCACGGTGACTCACCTGTATTCCTCCAGCATTTTGGGAGCCGAGGTGAGCAGATCACTTCAAGCTCAGGAG
TTCGAGACAGGCTGGCCGCAACATGGAGAAACCCCTCTTACTTAAATAACAAAATTAGCCCAAGGAGTGTGGC
AGTGTGCTGTATCCAGCATCTCAGGTGGTGAGCCAGGAGAATCGCTGAATCAGAGGGCGGAGGTGCACT
CAGCTGATGTGACCCGCTGCACTCAGCGCTGGGTGACAGATAGACATCTGTTTCAACAAACAAACACCGGAGG
GGGGTAGATAGCTGTTCTGCAACCTCTTAATCTTGATCTCTTCTTCAGGGTGCCCTGTATGTGGGGCTGT
GCAATCTCTGAGCAGGCTCCAGCCCGGAGGACAAGGAAGAGGCAATATTAGAGGGGCAAGAGTGTGAGCCGCC
GTGTGATATGATGCTCCGCGGAGGGGTTCTTCTGGCTGCGAGGTTGTGTGACCTTACCTCGAAACACACA
AAGAGCAGCATCTCAGATCTCTTGTGTAATGTGCTCCCTGCTCCCTCAGCTCCACCTAGGGCTCTCTGTGGGCC
ACTCTTGCTAGCTTGGGGTGCTGGTGCACTGCACTGCGGCGGTGATCCCTGGATGTTCTCTGCCCCCTCA
GTGTGGTGCCAGATCCGGCCCTGTGATAGCCGCGCTGTGCTCTACCCGAGGGCTACCACTGTGGACTGCAATGA
CTTATTCTTGACGGCATCCCCCGGCATCCCGCAGGCAACAGACGCTGTCTGTGAGACAGCAAGCATTTGT
CCGTGTGGAACAGATGAGCTGGGCTACTTGGCCATCTACAGAGCTGTGACCTGTCCAGAACAGCTTTTGGGA
TCCCGAGGTGTGATTTCATGCTGCCACGCTGTAGCTGTGACCTGTGAGGAGAACAGCTAGCCCGGCT
GGAGGACACAGCTTCTGTAGGGCTGGCCAGCTCTAGGAACCTATTCTCAACCAACACAGCTATCCGCACTGCG
CCCGAGGCGCTTTTGTGCTCAGCACTGTGTGGGCTGCACTCACTCAACCTCTGTAGGGCGACTTGAACAG
CCGCTGTTTGAATGTGCCCACTGTGAGATATCATGATTTGGCGGCAACAAGTGTAGATGTCATCTGGACAT
GAATCTCCGSCCTGGCCACCTGCTAGCTGTGTGTGATAGGACTGAACCTTGGGAGAGTCTCTGCAATATGTC
CTTGAGGGGCTGCAAAAGCTGGAGAGCTCTCTCTTCTATGACACACAGCTGTCCGCGGCTGCCAGCGGCATCT
GGACAGGCTGTCGCCGGCTCAAGTTCTTAGACTCAACAGAACCCGCTCAGGGGGTAGGGCGGGGAGCTTTGTC
CACATCTGTCTCACTTAAGAGCTGGGACTGACAACTACCAATAAACCCGCTGTCTTCACTCAACCCCGGCTTCA
GAACCTGCCCGAGCTTAAGAGCTGGGACTGACAACTACCAACACCCCTCAGTGTCTTGTGACAGAGACGCTGGAGT
CAACCTGCCCGAGTGTGAGAACCTCACTGTCTCAACACACAGCTTGTGCTTGTGACAGAGACGCTGGAGTCT
CTTGGCCCAACTCTCAGAGAGGTAGTGTCTCAGCCGCACTCAACCTGTGTGTGCGGAGCTCCGGAACCCGAGATCTACT
CAGGGGACCCGCTGTCTGCTCATGAGCCGCACTGTTGTGCTTCACTCCCAAGAGCTTCCCCCGCTCC
GGTCCGTAGGTCGCTTCTCCGGAGATGAGCGAGCATGCTGTGATTTGGCCGCACTGGCCGAACCCGAGATCTACTGT
GGTCACTCAGCGTGGGCTTCTGACTGCACTGCCCATCAGGACAGAGATCCGGGTGTACCCGAGGGGACCT
GGAGCTTCCGAGGTTGACAGCAGAGAGGAGCGGCTATACATCACTGTGTGTGSCCGAAGACTGTGTGGGGCTGACAC
TAGAGCGGTTAGTGTGTGTGTGGGCGCTGTCTCTTCCAGCAGCGCAGGAGCAAGACAGGGGTGTGAGCTCCG
GGTGCAGGAGAACCCACCTATCACTCATCTGTCTGTGTGCTCAACCCCAACAGTGTCCACCACTCACTC
CTAGCTCCAGTGCTCTCTCTCTCCGGGCGAGGGGSCACAGCTCTGGCCCGCTCCCTCGGGGAACCAAGCT
CACATTTACCCGCTCTTCAGGACAGGAGTCTGGGCTGTGCTCAGAGGCTTAGGGGATGTCTGGGCTCAT
TGGCATCTGGGCTCTGACTGTCTTCTTGGCAGCTGGGCTGAGCGGCCACTTGTGACAGGCACTGTGCTGGGCTGT
GGTGTGGGTGGGAGGGCGGCTCTCTCTCAGCTGGGCTTGTGGGCTGGAGTGCCCTCTGTGTGGGTTGT
GTGTCTCTCCCTGTCTCTCGTGAATCTCAGGAGGAGGCTGCCAGATCTCAGAAGGGAGACATGTGTGCC
ACATTTGTCTCAAAATTTGAGAGCTCAGGCTTCTCAGACATGAGAGAACTCACTAGGACTTTTATCAACA
AGAGAGCAGTCTGGGCAAGATGCTCCCTCGAGGAAGGGACATGGACACAGTGTCTGTAGGCTTGGCAGCTGGGC
CAGACAGCAATGGGCTTGTGTGCCCTGGGGTGCTTCTGACGCTTGAAAAAAGTGTGCCCTTCTCTAGGGTCA
CCTCTGTGTGCAATCTGAGAACTATCTCAAGGAAGAGGAGGACTTGGCTAGAGGCTTCTGCTCTCCCATTCT
CTCTCTGCGCAGAGGCTCTGGGCGCTGCTTGGCTGCCCTACTGTGTGCCGGGTGAGGAGGCACTTCATCTCAC
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCAGATCTGAAGAGATTTGGGAGAGGGATGTCCCGAGGA
CGCTCATCTCAGCAGCTGGGCTGGCATCTCGAAGTGTACTTCTATAGCAATTTGTACTTTGTGTGGAGAA
ATGTGTCACTTCCCCAACCCGATTCATCTTTCTCTGTTTTGTAAAAATAAAAAATAATAAACAATAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQLQNSIVRVDQSELGYLANLTELDLSQNSFSFDARDCDFHALPQLLSLHL
EENQLTRLEDHSAFGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNIETILMIGGNKVDAI LDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGPKFLDLNKNPLQRVGPGDFANMLHLKELGLNMMEELVSIKPFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLPQMETMLNNAALSAHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRVFI EPQSTLCAEPPDLQRLPVREVFPREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGRLRTPAHAGRRYRVYPEGTLELRRVTABEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYHILLSVWVTPPNTVSTNLTW
SSASSLRGQATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGRRPLPPAWAFWGSAPSRRVY
SAPLVLPWNPGKRLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGSAGGGGGACATTGTGTACCGCCT
 CTACATCGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGCTACACCGCTCTACTACGTGCAACAA
 CATCAAGTTTCGAGCTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
 CCTGGCCACACTCTTCAAGATCTCGCGCTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTGA
 CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAAGTACTCGTTTGAGTCGATCCGCTGAGGGAGAGCAGCTACAG
 CGACTCCCGCAGCTCAAGAACGACTTCGCCTTCATGCTGCATCTCAITGACCAATACGACCCTGCTTACTTCCAA
 GCGCTTCGCGCTCTTCTGTCCGAGGTGAGTGAGAACAGCTGCGGCAGCTGACCTCAACAAACGAGTGGAGCGT
 GGACAGCTCCGCGCAGCGCTCACCAAGAACGCGCAGGACAGCTGGAGCTGCATCTGTTATGCTCAGTGGCAT
 CCCTGCACCTGTGTTGACCTGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCGAGAGTCCGCTGTGCATCCCGCC
 CAGCATTCGCCAGCTCAGGGCTCAAGGAGCTGTGGCTTACCACACGCGGCCAAGATTGAAGCGCTCGCGCT
 GCGCTTCGCGGAGAACCTGCGGGCGCTGCACATCAAGTTTACCGACATCAAGGAGATCCGCTGTGGATCTTA
 TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAAACCGCTACATCGTCATCGA
 CGGGCTCGGGAGCTCAACGCTCAAGGTCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
 AGATGTGGGCGTGACCTGCAGAACTGTCTCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
 GAAGATGGCGAACTGACTGAGCTGGAGCTGATCCGCTGCGACTGGAGCGCATCCCCACTCTCATCTTCAGCCT
 CCAACACCTCGAGAGATTGACCTCAAGGACAAACACCTCAAGACCATCGAGGAGATCATCAGTTCCAGCACCT
 GCACCGCTCACCTGCTTAAGCTGTGGTACAACCATCGCTTACATCCCCATCGAGATCGGCAACCTCACCAA
 CTTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCCGAAGCTGGC
 CTACTTCGACCTCAGCAACAACCTGACCTTCTCTCCCTGCCGACATCGGCTCTTGCAGAACCTCCAGAACCT
 AGCCATCAGCGCAACCGGATCGAGAGCTCCCTCCGGAGCTCTTCCAGTCCGGGAGCTCGCGGCTCCGACCT
 GGGCAACACGCTGCTGCAGTCACTGCCCTCCAGGCTGGCGAGCTGACCAACCTGACGCAATCGAGCTCGCGGG
 CAACCGCTGGAGTCCCTGCTGTGGAGCTGGCGAGTCCCACTGCTCAAGCGCAGCGGCTGGTGGTGGAGGA
 GGACTGTTCACACACTGCCACCGAGGTGAAGGAGCGGCTGTGGAGGCTGACAGGAGCAGGCTGAGCGAG
 GCGCGCCAGCAAGCAAGCAGGAGACCGCTGCCAGCTCTCAGGCGCGGAGGGGCGAGGCTAGCTTCTCCAG
 AACTCCCGGACAGCCAGGACAGCTCGCGCTGGCGAGGAGCTGGGCGGCTTGTGAGTCAGCGCAGAGCGAGA
 GGACAGTATCTGTGGGCTGGCCCTTTTCTCCCTTGAGACTCAGCTCCCCAGGGCAAGTGGCTGTGGAGGAG
 AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCCTCGGAGCGAGCTCTCGCCACAGGGGCTGAG
 CTGCCACAGAGGCTCTGGGACCTCTCACTTAGTTCTTGATTTATTTTCTCCACTCCTCAGCTCTCTCATCC
 AGATAACTTATACATTCCCAAGAAAGTTTCAAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGGCTGCTCTTTCC
 TTGTCTTATTTAGCGATGCGCGGGGCTTTAAACCCACCTGGACTTCAGCAGAGTGTCCCGGGGCAACAG
 CCATGGGACGCTCACCCAGCAGTGCCGGGCTGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCTCCAGCTGGA
 AAGGCGAGGCTGGAGCTTGCCTCTCAGTTTTTGTGGCAGTTTATGTTTTTGTTTTTTTTTTTTAAACAAA
 AAACAAATTTTTTTAAAAAAAGCTTTGAAAAATGATGTTTGGGTATTAAGGAAAAAAGGCTTTAAAAAA
 AAAAGACACTAACGGCAGTGAAGTTGGAGTCTCAGGCGAGGTTGGCAGTTTCCCTTGAGCAAGCAGCCAGAGCT
 TGAATCTGTGTTCTCTTCCCTGGGCGCAGGCTGCAAGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
 CTATTGTTCTTGGGGAGGAGGTTTTTTGTTTTTTTTTGGGTTTTTTTTGGTGTCTTTCTCTCTCC
 ATGTGCTTGGCAGGCACTCATTTCTGTGGCTGTGGCGCAGAGGGAATGTTCTGGAGCTGCCAAGAGCAGACCTTA
 CTTGGGTTGGCTAATCCCGGATGAACGGTGCTCAATTGCACTCCCTCCTCGTGCTGCGGCTGGCTTCCA
 CGCACAGTGTAAAGGAAAGAGGAGGCACTTCGCCAGACTTTGTTTCCCACCTCCTCGCGCATGGGTGTGT
 CAGTGCCACCGCTGGCTCGCTGCTTCCATCAGCCCTGTGCCACCTGCTTCAAGAGAGCAGACACTTA
 GAGGCTGTGCGGAAATGGGAGGCTCGCCCTGGGAGGGCAGGCGTTGGTTCAGAGCCGCTCCCGTCCCTGGCG
 CTGGAGTGCACAGCCAGCTCGGCACTGGTGGCTGGAAGCCAACTGCTTTAGATCACTCGGCTCCCACTCT
 AGAAGAGCTCCCGCCTTAGATCAATCAGTGGACACTAAGGCAGCTTTAGAGTCTCTTGTCTTAATGATATGT
 CCATCGCTGTGTCGTCATTTGTCTTTCTGCGTGTGTCATGGATAATCTCAGAAATATGCAACACTAG
 CCTCTGACAACTGAAGCAAAATCCGTACATGTGGGTGAACTTGTAGACTCGGTACAGATCAAATAAA
 ATCTATAACAGAAAAA

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FIGURE 88

MRQTIIKVIKFIILICYTVYYVHNKFDVDCTVDIESLTGYRTRYCAHPLATLFKILASFYI
SLVIFYGLICMYTLWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLEHLFMLSIGIPDVTVFDLVELEV
LKLELIPDVTIPPSTIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI
YSLKTLEBLHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTVDVGVLQKLSI
NNEGTKLIVLNSLKMANLTELELIRCDLERIPHSIFSLHNLQELDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYDLSSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCA**ATG**GAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCGCTGAACGCAGGAGCTGTCATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACTTTGAGGAAATTGGGC
CCCTTGACAGTGTCTCAAACACGGAACACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACGTGGGTTCACTTATGTGAATGGTAGTGGTGCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCCATGAGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTACAGCAGGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTCGATCTCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTAACATAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTGACGCG
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGCCCTG
GGTGCAGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCACAGAACCTTGCTTTT
TACTGGATTCTGAAAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAA**TAG**GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAAATTATTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGGATCAAAATAAAGGATGATAATAGATATTAA

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Signal sequence:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAAGCTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGGCCACCGCTGGG
CACTCACGGCGGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTGAGTTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAAGGATGCCGTGCTTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGCTACACCAATATCAGCCACCCTTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTGTTGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 92

MGARGALLLALLLARAGLRKPKESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKG
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
CTTTGCCCTCATCTCTCTGGCAAAATGCAGTTACAGCCCGGAGCCGACCGGAGCGGAGCGC
TGCCCCAGGCTGGGTGTCCTTGGGCCGTGCGGACCCCTGAGGAAGAGCTCAGTCTCAGCTTT
GCCCTTGAGCAGCAGAAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGATCCAG
CTCTCCTCAATACGGAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCCACACGGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGTCTGGCTGAGCATCCGACAAGCAGAGCTGCTGTCTCC
TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAAGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
TTTCCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAAGGTGACAGGACTGTAGGCCCT
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTCAACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTCACATCAGGCCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCCTACATCCAGCGGGTCA
ACACTGAGGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCGCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAAGTTCGCCCTACCTTCCCTGCTCCAG
CCCCATGTGCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCACAATGA
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACCGCCCTTCATACCAGGAG
GAAGCTGTAAACGAAGTTCTTGAGCTCTAGCCCCACCTGGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGGCCATTCCATGGGTGTCCGAACCTCGGCCCTTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAAACCGTGGCTGCCATGAGTCTCTGT
TGGATGAAGAGGTAGAGGCCAGGGTTCTGTCTGTGCTGGCTGGGATCCTGTAAACAGGC
TGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTCTATC
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATCTGCGCTGTG
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCTTAGATTCTCAATAAGATGCTGTAACCTAGCATTTTGAATGCCTCTCCCTCCG
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCATTTCCCAATTCAGTGCAGGAGACCTCTACTGTACCGTTTACTCT
TTCTACCTGCATCAGAAACAAATGGCCTCCAGTGCATACCTTCAATCTTTGCTTTATG
GCCTTTCCATCATAGTTGCCCACTCCCTCTCTTACTTAGCTTCCAGGTCTTAACCTTCTCTG
ACTACTCTGTCTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTTTTGCCTTTCTCAGTTTACTCATTTGCCCTGGAAACAAATCACTGACA
TCTACAACCATACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
TGTA

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FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLLENVADLVRPSPLTLHTVQKWLLAAGAQQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGSGTSNNSQACAQFLEQYFHSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPTVGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCCGGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGTCTCGGCATGGCAGGGATTCCAGGGCTCTCTTCTCTCTC
TTCTTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCTTGGAAACCCACTGTG
GCCTGCATACCGCCTCCTGTCTGTCTTGCCCCAGTCTACCCCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCTAAGGGAAGT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTTCAGCATTTTTGGGAAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCTGGTGGCAGAGAAGCATGTCCTCACAGCTGCCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCTTAAAGCCC
AAGTTTAAAGATGGTGGTCGAGGGGCCAAGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTCTC
TGTTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATGGCATTTTTTCAGG
GCACCAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCCTATTTTAGGAGAGGCC
AAATTGTTTTTGTTCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGAAGGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAAGTGT
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA
AAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTGATTTTTATTTCATCTGAACCTGTTTCAAAGATTTATATTAAATATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAA

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Signal sequence:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCTTGGCTCTCGGTCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCTCAGACCCTGCAGAAGCTGAAGGTTCCCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGCGGAGGGCTGTGCCGAGCGCAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCCGTAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTTGTAACCTGCCCCACATATCTTATTTATTCCTCCAATTTCAATAAATATTATTAT
CTCCAAAAA

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FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCGCCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
AACAAGGAGCGCGGGCGCGCGGCAGAAATCTGTTGCCATCAGACAGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGC CAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTTCGCGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCGCTTACCTGGTAACAGAGGCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAACCCAGGCC
CCAACCTTCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCGCAAAATCGACCCATGTTCCCTATCCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCTCCAAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGGTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTGTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACCTCAAAGGG
TGAAGAGGTGAGCTGTCTCTGTGTCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCAACAAGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGGAAGGAAAGTAACCTCCTGACTCTCCAATAAAAACTT
GTCCAACCTGTGAAA

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FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPGVGTDEEKRMLMVELHNLRYRAQVSPASDMLHMRWDEE
LAAFAKAYARQCVVGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLVVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLFYLVTAPSFRAATEASDSRKMGTPTSSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSV
SGLNSGPGHVWGLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

09904877.071201

FIGURE 101

GTAAC TGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTTATGCTGGACGT
 ACTCTGTGTTGTTCTCCCTCTGCTTGCTTTTTCACATAGCAGACCGGACTTAAGTCAACACGATATATCTTTTCAT
 CAAGGCACAGTTCCATGAGGCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACATGAATGGAGACCATTCC
 AAATCTGGGACAGCTTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAACACAGGATTTGTGAAATCTACCTCGTGA
 ACATCTGAAGAGTTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCAAT
 TCCAGCCCTACAGCTCAAAATATCTGATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA
 TTTGGCCCAACACATCTCTGTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACT
 GCCCAACTGCAACATCTCGAATTTGAACCGAAACAGATTTAAATGTAGATGACCTGACATTTCCAAGGCTTGG
 TGCTCTGAAGTCTCTGAAATGCAAGAAATGGAGTAAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA
 CATGGAATTTTTCAGCTGACCAATAACAACCTAAACAGAGATTAACCAAGGCTGGCTTTACGGCTTGTGATGCT
 GCAGCAACTTCTACGACCAAAATGCCATCAACAGGATCAGCCCTGAGCTTCCAGTGTTCAGATTTAAAGACTTT
 TGAGCTGGACCTTAACCTTCAATCACTTATCAAGGTTAGATGATTTCAAGCTTCCCTGGCCCTTAAGCTTACATAATAC
 ACTGCACATTTGGGAACAACAGAGTCAGCTACATTTGCTGATTTGTCCTCCGGGGCTTTCCAGTTTAAAGACTTT
 GGTATCTGAAGAACAAATGAATTTTCTGGACTATTGAAGACATGAATGGTCTTTCTCTGGGCTGACAACTGAG
 GCGACTGATCTCCAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTTGGAGCA
 TCTAGACCTGAGTGCAACCAATCATGTCTTTTCAAGCCATGCAATTTTCAACAAATGAAGAACTGCAACAAAT
 GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAATGGCTCCCAAGTGGGTCGCGAAACAACTT
 TCAGAGCTTTGTAATGCGAGTTTGTGCCCTCTCAGCTGCTAAAAGGAAGAACATTTTGTCTGTAGCCGAGA
 TGCTTTGTGTGTGATGATTTTCCAAACCCAGAGTCAGGCTTCAGCGAGAACACAGTCGSCAATAAAGGTTT
 CAATTTGAGTTTCACTGTCTCAGCTGCGCAGCAGCAGTGATTTCCCAATGACTTTTGTCTGGAAAAAGACATGA
 ACTACTGCATGATGCTGAATGGAAAAATTATGCACACCTTCGGGCCCCAAGGTGGCGAGGTGATGAGTATATACCA
 CATCTTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCACTGTGCTCACTTCAATCTTGGTTT
 ATCCCTACTCTGTCAAGACCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGATCTCACCAT
 CCGAGCTGCGGGCACATGGCAGCTTGGAGTGTGCTGTGGGGCAACCCAGCCTCCAGATAGCCTGGCAGAGGA
 TGGGGGACACAGACTTCCAGCTGCACGGGAGAGACGATGCTGATGTCGCGAGGATGACGTGTTCTTTATGCT
 GGATGTGAAGATAGAGGACATTTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAAGGAATTTTCAACAAATGC
 AACTCTGACTGCTCTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAAACCAAGGGAGAACAGC
 CSTCCTACAGTGCATTTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCATTTGTGGT
 AACCGAGAGGCACTTTTTCGACAGGCAATCAGCTTCTGATTTATGTGACCTCAGATGTCAGTATGCTGGGAA
 ATACACATGTGAGATGCTAACACCTTGGCACTGAGAGAGGAACAGTGCCTCTCAGTGTGATCCCCACTCCAC
 CTGCGACTCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAGC
 CGTGGTTTGTCTGTGGTGGGCGACGTCATCGTGTGGGTGCTCATATACCAACAAGGCGGAGGAATGAAGA
 TTGCAGCATTAACAACAGATGAGACCAACTTGCAGCAGATATCTCAGTATTTTGTCACTCAGGGAACGTT
 AGCTCAGAGGAGGATGACGTGCTTTCAGAAAGTGGAAGCCCACTGATTTTGTGCATCTTCACTTCCAGGTGCTGG
 ATTTTCTTACCAACAATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAGCTGC
 CACAGATCTGTTCTTTTGTCTGCTTTTGGGATCCACAGGCCCTATGTTTATGAGGGAAATGTGTATGGCTCAGA
 TCCCTTTTGAACATATCATACAGGTTGCACTCTGACCCAGAAACAGTTTAAATGGACCACTATGAGCCACGTTA
 CATAAAGAAAAAGGATGATACCATGTTCTCATCTTCAAGAAGTCTGCGAACCGAGCTTCAGTAATATATC
 GTGGCCCTTCATGTGAGGAAGCTCACTTAACTAGTTACTCTCAATAGGAAGCTTGAATGAAAAATCTGTG
 TCTAAACAAGTCCCTCTTGTAGTTTATGTGCAAAATCCAGAGCCAGCGTGGTGGCTCGAGTAATCTTTCATGGG
 TACCTTTTGAAGATCTCTCAGGAGACCTCACTAGATGCTTATCAAGCTTTGGACAGCCATCAGATTTGTCAGCC
 AAGAGCCTTTTATTTGAAGCTCATTCTTCCAGACTTGGACTCTGGGTGAGGAGAGATGGGAAGAAAGGAC
 AGATTTTCAGGAAGAAATCACTATTGTACCTTTAAACAGACTTGAAGAAATACAGGATCTCAAAATTTTCAGTC
 TATAGACTTGGACATAAGACTGAAATGAGACCAAGGAAAGCTTAACTACTACTCTCAAGTGAACCTTTTATTTA
 ATAGAGAGAGAATCTTATGTTTAAAAATGGAGTTATGAATTTTAAAGAGATAAAATGCTTTTATATACAGAT
 GAACCAAAATTAACAAAGTTATGAAATTTTATACTGGGAATGATGCTCATATAGAATACCTTTTAAACTA
 TTTTTTAACCTTTGTTTATGAAAAATGATCTTACGTAAATTAATGATATAATCATGATATTTTATGATTTT
 TTATAATGGCAGATTTCTTTTATGAAAAATGAGTTACTAAAGCAATTTAAATATACCTGCCCTGTACCAATTT
 TTAATATGAGTATCTCATATATTTTGCACATTTATTTTAAATAAATGCTGCCCTGTACCAATTTGAA

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FIGURE 102

MVDVLLLFSLCLLFHISRFDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEITLPEHLKEFQSLETLDLSSNNISELQTAFPAQLKLYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAI PPKMFKLPLQLHLELNRRNIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDWE
FCQKLSLELDLTFNHL SRLDDSSFLGLSLLNLTHIGNNRVSYIADCAFRGLSSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSI TTKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPLQWVAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNDLHDAEMENYAHRAQG
GEVMEYTTILRLREVEFASSEGKYQCVISNHFSSSYSVKAKLTVMNMLPSFTKT PMDLTIRAGA
MARLECAAVGHPAQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETA V LQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVSDSDV DAGKYTCESNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIIAVVCCVVGTSLVVVV IYHTRRRNEDCSI T NTDETNLPADIPSYLSSQGTAD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTC HIDSSEADVEATD LFLCPFLGSTGP
MYLKGNVYGSDFPETYHTGCSDPDRPTVLMHDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD F SANPEPASVASSNSFMGTGFKALRRPHLDA
YSSFGQPSDCQPRAFY LKAHSSPDLDGSGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCACCTTTCTCCGGAACCGAACCAATGGGATAAATGATTTGTGCAAGAGAGAAGGAGAAC
GAAGCTTTTTCTGTGGGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCATTCAGGAATGAAA
TAAACAGAGTTAGACCCCGGGGGTGGTGTCTTGACATAAATAAATAATCTTAAGAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTTCATTTTTCTC
TATAAAGGAGAAATGAGCAAGGAGATATTTTTGGAATGAAAGTTTGGGGCTTTTTAGTAAAGTAAAGAACT
GGTGGTGGTGTCTTTTTCTTTCTTTTTGAATTTCCCAAGAGGAGAGAAATTAATAATCATCTGCAAGAGAAA
TTTCAGAGAGAAAGTTGACCGCGGCAGATTGAGGCATGATTGGGGGAGAGAAACAGCAGCAGCACTGTTGGA
TTTTGTGCTATGTTGACTAAATGACGGATAATTGCAGTTGGATTTCCTTCATCAACCTCCTTTTTTTAAAT
TTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACCACTGGATTTCATCTGGATGTGCT
GTGATCAGCTGAAATCAACATGTTTGAATTCAGAGAGGACCAACACAGATAAATATGATATGTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGCCCTTATTGACCCCTGCTGTGGTGGT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
CCAGTTCCAGCAAGTGATTTGTGTTCCGAAAAACCTGCGGAGGTTCCGGATGTCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAATCCAGTCACTCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTTGGAAATCCT
ACAGTTGAGTAGGACCATATCAGAACCATGAAATTTGGGCTTCAATGCTTGGCGAACCTCAACACTCTGGA
ACTCTTGACAATCGCTTACTACCATCCGAAATGGAGCTTTGTATCTGTCTAAACTGAAGGAGCTGGTT
GCGAAAACACCCCATTTGAAGCATCCCTTCTTATGCTTTTAAACAGAAATCTCTCTTGGCGGACATAGACTTAG
GGAATTGAAAGACTTTTCAATCATCTCAGAAGGTCCTTTGAAGGCTGTCTCAACTTGAGGTATTGAACTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAATGATAGCTGAGTCTTTCTGGGAATCA
TTATCTGCATCAGGCGCTGGCTTCTTCCAGGGTTTGATGCACCTTCAAAAATCTGGTATGATCAATCCAGAT
TCAAGTGATTGAACGGAATGCCCTTGACAACTTCAGTCACTAGTGAGAGATCAACCTGCACACAAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACAACCTTGGAACTG
TAACTGTGACATCTGTGGCTCAGCTGGTGGATAAAGAGATGGCCCTTCCGAACACAGCTTGTGTGGCCGCTG
TAACTCTCTCCCAATCAAAGGGGAGGTACATGGAGAGCTCGAGCCAGAAATTAATTCATGCTATGCTCCGCT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCTGGCAGCTGAGCTGAAATGTGGGGCTTCACATC
CCTGACATCTGTATCTTGGATTACTCCAAATGGAAAGTCTGACACATGGGGCGTACAAAGTGGCGATGCTGT
GCTCAGTGATGGTACGTTAAATTTCAAAATGTAAGTGTGCAAGATACAGGCATGTACATGTATGGTGAGTAA
TTCGTTGGGAATACTACTGCTTCAGCCACCTGGAATGTTACTGCAGCAACCACTACTCCTTCTTCTTACTTTTC
AACCGTCAAGTAGAGACTATGGAAACCGTCTCAGGATGAGGACGGACCAAGATTAACATGTGGGTCCCACTCC
AGTGGTGCAGTGGGAGACCAACCAATGTGACACCTCTCTCACACACAGAGCAAGGTCGACAGAGAAAACCTT
CACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATAT
TGGGTGTTTTGTGGCCATCACTCATGGCTGCAGTGATGCTGCTCATTTCTACAAGATGAGGAGACGACCA
TCGGCAAAACCATCACGCCCAACAGGACTGTGAAATTTAATGTGGATGATGAGATTACGGAGACACACC
CATCGGAAGCCACTGCGCCATGCTGCTATCGAGCATGAGCACTAAATCACTATAACTCATACAAATCTCCCTT
CAACACACACAAACAGTTTAAACAATAATTCAAATACAGTTTCACTGATGATGAAACCGTTATTGATCCGAATGAA
CTCTAAAGCAATGTACAAGAGACTCAAACTTAAACATTTACAGAGTTTACAAAAACCAACATCAAAAAA
GACAGTTTATTAATAATGACACAAATGACTGGCTAAATCTACTGTTTCAAAAAAGTGCTTTTCAAAAAACAA
AAAAAGAAAGAAATTTATTTATTAATAATCTATGTGATTAAAGCAGACAAAA

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FIGURE 104

MLNKM TLHPQQIMIGPRFNALFDPLLVL LALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSK LKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNRLRYLNLAMCNLREI PNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIH LHHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTGMYTCMVSNVGN
TTASATLNVTAATTTFFSYFSTVTIVETMEPSQDEARTTDNNVGTPPVVDWETTNTVTTSLTPQ
STRSTKTFITPVT DINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

05047-0721

AGGCCAGCGCTGCTCAAGCTCAACATCTTGCTGTGCACTTGGCGAGTTCTTTTTCGTTTCCCTCTCGTGTGTTTGGGGGCA
TGAAGAGGCTTCTCCGCGCGGATTAAGAAAGAAATTAGACGGCAGCGCGAGGAGAGCGCCACGCGAGCGCTC
GAGGCGCGCGCTGCTCACTCTCGCTTGGAAAGTTTGTGCCCGGCCCCGACGCGCGCGCGCTGGGAGCTTTCGGGTAGA
GAACTAGGCGCTTGACCCCGCTAGTACGCGCGCCAGCTCTCGTGTCCGCGCGCGCGGGTTGGGGCTGTCTCTGTG
CGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGCTCGCGGGAACTCGGCGAGCCCTCTTGGGCTGACGCGCC
GAGCGCCCATCGCCCACTACCTCTGCCGCTGCTCGCTCGGGAGCTCTGTGAAGTCGAGTCTGTAAAGCGGTAGCGGCTCT
CTCGGAGCACTCTCCGTGCTGGTGTGCTGCGGTGGACTTAAGTACACACAGATATTTCTTCACTCAAGGCAAGTCTTC
ATGAGCCCACTCTCAAGGCTCTCGAGAAGGTGAATCAAGAACCAATGAATTTAGAGACCACTCCAAATCTGGGACGAG
TCTCGGCAATATATACACTTCTCTCTTGGCTGGAAACAGGATTTGTGAATATCTCCTTGCAATCTGAAAGAG
TTTCAGTCCCTTGAACCTTTGGACCTTACCGAGTACACAAATATTTCCAGAGTCCAAATCTGATTTCCACGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTACACATCAATGGAACCTGGGTATTTTGAACATTTGGCCCACTACAG
CTCCTTTGTTTAAAGCTGAACAGAGAACCAATCTACGTTATCCCAACCAAGATTTTAAACCTGCCCAACTGAAAT
ATCTCTGAATTTGAACCGAACAGAACTAAAAATGTATAGTACGTACATCTCAAGGCGCTTGGTGTCTCTGAAGTCT
CTGAAATTCGAAAGAAATGGATGTACGAAGAACTTATGGATGAGGCTTTTGGGGCGTAGCAATGGAAATTTTTC
CAGCTGGACCTTAAACACTTACACAGATATTACCAAGATTCACCAAGCTTGCTTTACCGGTCTGTGATGCTCGAGAACTTAC
CTCAGCCAAATTCGCACTCAACAGGATCAGCCCTGTATGCTGGGATGTTCTTGGCAGCACTCAGTGAAGCTGGACATCTAC
ACTTTCAATCACTCTCAGGTTTGATGATGATTTCAAGTCTCTTGGCTTACGCTTACTAAATATACAGTGCATCTGGG
AAACACAGAGTCAAGCTACATGCTGATTTGGTCTCCGCGGGCTTTTCAGTTTAAAGACTTTGGATCTGAAGAAC
ATGAATAATTCCTGGACTTATGAAGACAGTAATGTGTGTTCTCTGGGCTTGACAACTGAGGCGACTGATCTAC
CAGGAAATTCGGATTCGTTTATTATTAAGAAAGCTTCTACGTGTTTGGATGCTTTGGAGACTTACAGCTCTGAGT
GACAGCGCAATCTATGTTCTTCAAGGCAATGTCACTTCAAAATGAAGAACTGCAACAAATGCAATTTAAATACA
TACGAGCTTTTGTGCGATTGCGCAGTAAATAGTCTCCACAGTGGGTGGCGGAAACCAATTTCAGAGCTTTGTAT
TTCCGCGAGTTTGTGCCATCTCAGCTGTCTAAAGGAAGAAGCAATTTTGTCTTGATGCCCAAGTGGCTTTGTGTGT
GATGTTTTCCTCAAAACCCAGATACAGGTTTCAGCCAGAACACAGCTCGGCATACGCGCAATTAAGAGTTTCCAATTTGAGTTTCT
ATCTGCTCAGCTGCGACGACGATGATTTCCCAATGACTTTGCTTGGAAAGAAGCAATGAATCTGATCTGATAT
CTGAAATGGAAATATGCACTACCTCCGGGCCAAGTGTGGCAGAGTGATGAGATACCAACCATCTCTCCGCTGT
CGGAGGTTGGATTTTCCGATGAGSGGAATATCAGTGTGTCAATCACTTTGGTGTCTATCTACTCTGTCT
CAAGCCAGCTTTAGCTAAATATGCTTCCCTCATTCACCAAGACCCCATGATCTCAGCATCGGAGCTGGGGCC
ATGGCACTTTGAGTGTCTGCTCTTGGGCACTGACGCCCCAGCAATGCTCAGCAAGACTGGGGGACAGAGT
TTCACGCTCAGCGAGAGACATGCACTGATGTCGCGAGGATGACGTGTTTCTATCTGGATGTCAAGATA
GAGGCAATGGGGTTATACGCTTGCACAGCTCAGAACCTGAGGAAGTATGAGCAATTCGCACTCTGATCTGTC
CTAGAAAACACATCACTTTTTCGCGCTGTTTGGAGCGCACTGTAACTGGAGAGAAAGACGCGCTCTACAGTGC
ATTTCTGGAGAGAGCGCTCCCTCTAACTGAATCGACGCAAGATGATAGCCATTTGGGAAATACACAGAGGCA
TTTTTTTTCAGCAGCAATCAGCTCTGATATTTGTGAGCTCAGATGTGATGTGATGTTGGGAAATACACATGTGAT
ATGTTCTAACCACTTTGGCATGAGAGAGGAAAGCTGCGCTCAGTGTGATCTCCCATCCAACTCGACTCGCACTCCCT
CAGATGACAGGCCCTACCTGTAGACAGTACGAGTAGGGGCACTTGTGGGTGTCTGTATCATGCGCTGTGTTGCTGT
GTGGTGGGACGTCATCTGTGGGTGTCTATCATACACACAGCGGAGGAATGAAGATTCAGCATCTCAGCATCC
AACACAGATGAGACCACTTGCACAGGATATTTCTAGTATTTGTATCTCAGGGAACCTAGTGCACAGGCA
GTGGGTACGTTCTCGAAGATGGGAAGCACACAGTGTGTGCACTCTCAGGTGTGGCAATTTTCTTCAACA
CAATCATGCTGATCTGGGAGCTGCTCATATTGACAAATAGCAGTTGAACATCTTGGAGCTGGAATCTGTCTCT
TTCTGTTCGTTTGGGATCAGCGGCCATGATATTGTAAGGGAAGATTTGTGGCTCAGATCTTTTGAACA
TATCATACAGTTTGCATGCTTGCAGGCAAGAACAGTTTAAAGGCACTATGAGCCAGTTACATAAGAAAGAG
GAGTGTCCACCATGTTCTCATCTTTCAGAGAATCTCTGCAAGACGCGATCTCAGTAAATATATCTGTGGCTCTC
TGGAGGAGCTACTTAACTAGTTACTTCTCAATGAAGAACCTGGATAGAAAATCTGTGTACATAAGACTCT
CTTTAGATTTTATGCAAACTCCAGAGCAGCTCGGTTGCTTCAGGTAACTTCTTACGGGTATGCTTTGAAAC
GCTCTCAGGAGACTCAGTATGCTCATTTCAAGCTTTGGACAGGATCAGTTGTACGCAAGAGCCTTTTAT
TTGAAGACTCATTTCTCCCGAGCTTGGACTCTGGGTGAGGAGAAGTGGGAAGAGAGGACGATCTTTCAGGAA
GAAATACATTTTGTACTTTTAAACAGACTTTAGAANAATCAGGACTCCAAATTTTCACTTATGCTTGTGAC
CATATGCTGATGAGAGCAAAAGGAAGCTTAACTACTACTCTCAAGTGAACTTTAAAGAGAGAGAAT
CTATGTGTTTTTAAATGGAGTTTGAATTTTAAAGGATAAAAGCTCTTATATACAGATGAACCAAAATAC
AAAAGATTTGAAATTTTATATCGGAATGATGCTCATATAAGAAATACCTTTTAAACTTTTAACTTTG
TTTTATCAAAAAGTATTTACGTAAATTAATGATATAAATCATGATTTTATGATTTTATATATGCGGACA
TTCTTTTATGAAATAGATGATTAATTAAGCAATTTAAATAATCTCGCTGTTACCATTTTAAATAGAAAT
ACTCATATATTTTGACATATATTTAATAAATGTGTCAATTTGAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFTKASSMSHLQSLREVKLNNNLEETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLLETLDLSSNNISELQTAPPALQLKYLNLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIISAIPKMFKLPLQLQHLNLRNKIKNVDDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNTETITKGWLYGLLMLQELHLHQNAINRISPDWFEFC
QKLSLELDLTFNHLRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSSLKTLDLKNNIEIS
WTIEDMMGAFSGLDKLRLLILQGNRIRISITTKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNLTSSLLCDCQLKWLPOWVAENNFQSFVNASCAPQLLKGSRIFAVSPDGFVCDFF
PKPQITVQPETQSAIKGSNLSPICSAASSSDSPMTFAWKDKDNELLHDAEMENYAHLLRAQGG
VMEYTTILRLREVEFASGEKYQCVISNHFQSSSYSVKAKLTVNMLPSFTKTTPMDLTIIRAGAMA
RLECAAVGHAPAPQIAWQKDGTDFFAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETSPFLRPLLDRTVTVKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
FAAGNQLLLIIVSDSDVSDAGKYTCESNTLTGTERGNVRLSVIPTPTCDSPQMTAPSLDDDDGWA
TVGVVIAVVCVVGTSLVVVVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLDLRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNNVYSDPFETYHTGCSDPDPTVLMDHYEPSYIKKKECYPCHSPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSLLDFSANPEPASVASSNSFMGTGFKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDSSGEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

09904377 071201

090487284060

AAAAACTTGCCTCGCGGAAGGGCCGACCTTGACTTGAAATGGAGAGGACCGAGGCCGAGGAGCGAGCTAGAGAT
 TGGGGGACGCGCTTCGCGCTCTGTGGGCGCGCTCTCGCGCGCGGAGCGCAGCAGAGAGGGAAGCTGTGCTGCC
 CTGCTCGACGAGGCGCGCACTGTGTGAAAGCGGAGAGCGCTGTGTGTGGCAGCCGCTATCTCCCTTTATATAGA
 GAACCTCTTCCACATCTGGGAAGGCGAGCGGCGAGGCGAGGCGGCTCATGTGTGAGCAGGAGCCGCTGTCTGACAG
 GCGCAGCAGCATCTCGAGTATTACAGATTTTACAGATACCAATTGGGAAGGCGAGGAGCAGAACAGCCTGCTGTGT
 TGCATCAGGCCCTTGGCGCCGACGGCATCTGACTACCGCACCCCTTCAGGACACCATTGGCCACAGGCGGCTGTGCTG
 TGCTCTCGTGCTGTCTGCGCCACAGCTGACCTGGGACTGTGCTTTCGCTGAGGGCGCCAGGATTTTGGCCAGAT
 GTGGCGGCCACAGCTTGAGCCCGGAGAGCAAAATTTGCGGAGGAGGAGCGCGCTGTGTGATCTGAGCCCTGAGC
 AGCCCGGCGCTGGCCGACCGCGCGTCACTGTGCGCCAGAACATGTGCTCTCCAGAGGCGGTGTGGATCTGTG
 GCGGTATTGACTCTCGGTGATTTCGCGGGGACCTGCTGTGAGCAGACCAACCACTATCTTCAGGAAACCAACGAGT
 TGGAAAGATCTACCTCTGAGGAGTCTCTCCGGTTCGACCGGTGGAGACACTGAACTCGCAAAACCAACCGCTGAC
 CTTCGCGAGGGCTCCAGAGAAAGGCTTTGAGATCATGACCAACTCAATTATCTGTACTTGGCCAAATAACAAGT
 TGACCTTGGCACCCGCTCTCTGCAAAAGCGCTGATCAGTGTGGACTTTGCTGCAACTATCTACCAAGATCTCT
 ATGGGCTCACTTTTGGCCAGAAGCCAAATCTGAGTCTGTGTACTCTGCACAAACCAAGCTGGCAGACGCGGGGCT
 TCGCGGACAAAGTTTCAACGCGCTCGACAGAGTCTGAGGTCTCACTCTGTCGACAGACTCTCTCGCCGACGCTG
 CCAAGCACTTCGCGCTGCTGCTGTACAGAGCTGACCTCAAGAACACAAAGCTGGCAGAGAGATCGCCCGGGGGGCT
 TCGAGCGGCTGAGCAGGCTGCTGCGAGCTATCACTTCAGAAACAACTCACTGACTGACGAGAGGAGCCCTGCAGACGGA
 CTTTCTGGAAGCTCTCCAGCTCTGAGATGACTTGATCTGTGCACCAACCACTGTCTGGGCTCCAGCTGGGCTGCG
 CGCGCACTTGGTCTGTGCACTCTGTAGAAAGAAAGCCATCCGAGGCTGTGAGCGCAATGTGCTGACCCCACTCC
 CGAGCTCTGAGTCACTCTGCTGTCACAGAACACAGCTCGGGAGGAGGCACTCAACCCTGACCTCTCCAGGGCC
 TCAAGCGTTGCAACAGTGTGCACTCTGACAAACAGCGCTGGAGCGCTGCCAGTGGCTGCTTCCGCGGTGCG
 GCACCTCATGATCTTGCAACACAGATACAGGCACTATGGCCGCAAGACTTTGCCACCACTACTCTCTGGAGG
 AGCTCAAGCTCACTCAGTCAACACCGCATCAAGCGCCAGGTGACCGCGACAGCTCTCCGAGAGCTGCGCTGCTGCT
 TCGCTCTGAGCTGTCTGGGCAACCGGCTGCAACCGCTGCACTGGGCTGCCCTCGAAATGTCTCATGTGCTGAAGT
 TCAAGCGCAATGAGTGTGCTGCTTGTGCAACAGGAGCGCTGGCGGGTCAAGCTGCTGAGTCACTGACTCA
 CCAAGCAACCGATCGCGACCGGACGCTGGGCCCGCTGCGTGGGTGACCTTCGCACTTCGACTCTGCGCTGCA
 TCGCCGGCAATCAGCTCAAGAGATCCCGAGGGGCTCCCGAGCTCACTGGATGATCTTACTCTGCAAAACAA
 AGATTAGTGGGCTGCGCCCAACGATCTGATCTCAGCCGCACTCAAGGGATCTTTCTCAGTTTAAACAGT
 TGAGTCTGGGCTCGGTGTTGACAGTGCTCTTCGAGAGGCTGAAGCACTCTCAGGTTCTGTGACATTTGAAGGCACT
 TGAGTCTTGTGTGATCAATTTCAAGAGCCGTGGCCGCTTTGGGAGAGGAAAGAGGAGAGGAGGAGGAGGAGG
 AAGAGAGAGGAAACAGATAGTGTGACAGGTGATGATGATGTGACTTAGGATGATGAGCGCGCGGCACTCTTTTCTG
 AGCAACGCTCTGTGCTGTGAGCCGCCCACTTCGCTGCTGTGACAGACACACAGCAGCTGCACTATGAGGCA
 TCCCACTACATCAAGCGGCTGACAGCTGTCAATATCCCCACCCCTTCACAGGCGTGTCCACGCGCAGACATGAC
 ACACACATCAACACCTCAAAACCCAGCTCAGGCCACACAACTACCTTCAAAACCAACAGCTGTCTGTGACAC
 CCCCACATGACGCTGCAACGCTCTGAAATATGACGAGGAGAGGCTGTGCCCTGCTGCGCAGCAGGCGACCA
 TTCTCTCTCCCTCTGCACTGTGTGATGCTGATGATGACACACACACACACACATCAAGTCACTGTGTGCGAA
 CAGCCCTCCAAAGCTATGCAACAGCAGCTCTTTCGCGGACAGCAATGACGATAGCAGCTCGGCTCTGCCCTCT
 GGCATCTGCTCGCTCGTTCTCTGGAGAGACACAAGGATCTCATGCTCTGTGGCAGAGTGCTGCAACCTCT
 GGAATCTGCAAAAGCTGGCTTTTATCTCTTCCCATCTATGTAGGGGACAGGAGCTCTCAGAGTCTGTGCGCTGCCC
 TGGCCCACTCTGCTCTCAGGCTCTGGGACACTCTGTGATAGAGTCCCTCTCTGCAAGCCCTGTGGCAGGACA
 CAGGCACTTTTCAAATGGGCAAGCCCAAGTGGAGCGAGATGAGGAGAGCCCTCGGTTGCTGTGGGCGCTTGGGG
 CAGGCTGAAGCAGAGTGATGGGCTGGGCTGAGCGAGGAGAGGAGCCAGCTGCACTGTGAGAGACACTTTT
 GTTCTTCAGGCGCTGTGGGGAGATTCCGGGTGCTTTATTTTATTTTATCTTTCAAAGGAAAAAATGATAAAAT
 CTCAAAGCTGATTTTCTTTGTTTATAGAAAACATAATATAAAGACTATTCCTATCCCTGCAAAAAAATGATA

FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCGCGCGCTCGCCGCTGCTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGCGCAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGGGCCCTCCCATCGGCGCCACACCC
CAACCTGTTCTCGCGCGCCCTCTGCGCTGCGCCCGAGACCCTGCCCCAAGTGGATTCTCTCGCGCTGGT
GCTGGTATCCTCGCTCTACCTCGCAGGCGCGCCCGCAGTTTCGACGGGAGGTGGCCAGGCAAAATAGTGTATCGAT
TGCCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGAGCAGTGTACGCC
TGTGTGCCAACACAGCATGCAAACTAGTGTGAATGTATCGGGCCAAACAAGTGTCAAGTGTATCTCGTGGTTATGTCTGG
AAAAACCTGTAAATCAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAAGCAGGGTGCAATGAACAATT
CGGCAGCTCAAGTGCTACTGTCTCAACGGATATATGTCTATGCGCGGATGGTCTCTGCTCAAGTCCCTGACCTG
TCCCATGGCAAACTGTGATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCTGCCCTGGCCCT
GCACCTGGCTCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCTCCCTCGCCCTAGATT
TAGGCAATTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAAATATCAATGTCTAGACATAGACGAATGTCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTCGATGTTATAA
CGTACGTGGTCCCTACAAGTGCAAATGTAAAGAAGGATACCAAGGCTGATGGACTGACTTGTGTGTATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCAATGTACCAAGGGAATGTTACCAATTTTAAAGGGTGACACAGGAAA
CCTGCGCAACAGAGCTCAGAACACCTTACCACCTACAAACCCAGAAAGGCCAACACCGGACGTGACAACTATAGC
ACAGCTTGCCAGTACACTCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGCCCTCAGAAACCCAGAGG
AGATGTGTTCACTGTTCTCGTACACAGTTGTAAATTTTGACCATGGACTTTGTGATGGATCAGGGGAGAAGACAA
TGACTTGCACTGGGAAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGGCGACCAAGCCCCAGG
GGCAAAAGCTGACACCTTGGTGTCTACCTCTCGCCGCCCTCATGCAATTCAGGGGACTGTGCCCTGTCAATTCAGGCA
CAAGGTGACGCGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACCGGAGCAGCCCTGTG
GGGAGGAAATGGTGCCATGGCTGGAGGCAACACAGATCACCCTTGCGAGGGCTGACATCAAGAGCCGAATACAC
AAGATGATTAAAGGGTTGGAAAAAAGATCTATGATGGAAAAATTAAGAGCACTGGGATTATTAGCGCTGGAGAG
AGAAGACTGAGGGGCAACCAATGATGGTTTCAAGTATATGAAGGGTTGGCAGAGAGGGTGGCGACAGCTG
TTCCTCATATGCACTAAGAATAAGAACAGAGGAAACTGGCTTAGACTAGAGTATGAAGGAGACTTCTTGGCAGG
GGCCATGTGTAGAACTCTCATAAAAAAGGAAGTGTGAAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAGATGGTTAAGATGTTCTTACCAAGGAAAAGTAAACAAATATAGAAATTTCCCAAA
AGATGTTTGTGATCTCTAGTAGTATGCAAGTGAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CAATTCCTCTTGACCTCTTAATGGAGAGGGATTGAAAGGGGAGAGCCCAAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTTAGCAGTATTAAGAAAAAAGGAAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTTCAATGTTTCTTCATGTTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTCTTTTCTTAAAGAGATCTTCAAGGAAACAGAGTTCAAGAG
ATTTTCATCGGGTGCACTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGTGAGAAAGAGTGCCCTGCGCC
ACACCGGAGAGCTTCTCTTCACTCATCAGTATGATTCAGTTTCTCTTATCAATTTGAGCTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAACAAATAGGTACAAATAGAAGTCTTCTGTCAATTTAACTGGTAAAGGCGAGGCTGG
AGGGGGAATAATTAATTAAGCCTTTAGTAAACGGCAGAAATATAGGCTGTAGATCCAATTTTAAAGGTTCAAT
TCTTTTAGTGCATAACTGATGGAAGAGTTATCCAAAGTACTGTATACACTTGTGTTATTATTATTAATGTTT
CTAAAAATAAAATGTTAGTGGTTTCCAAATGGCCATAATAAAACAATTTTGTAAATAAAAAACACTGTTAGTAAAT

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FIGURE 110

MDFLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRQCPSPLHLAPDGRCTVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDEC SLGQYQCSSSFARCYNVVRSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGD TGNNWIPDVGSTWVPPKTPYIPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPOKPRGDVFSVLVHSCNFDHGLCGWIREKDN DLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRLMHSGDLCLSFRHKVTGLHSGT LQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCAATTTGCCCTTTAGATTGTGA
AATGTGGCCTCAAGGTCTTCACAACTTTCCTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGA
 AGGTGACAGTGGCCATCACACACTGTCATGGCGTCAGAGGTGAGGCCCTTACCTACCCGTC
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
 CACAATGCCCAAATACTTTACTGGGCTCTGTGAATAAGTCTGTGGTTTCTTGACTTGGAATACC
 AACACAAGTTCACCATGATGCCACCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT
 GATGAAGGCAATTACATCGTGAAGGTCAACATTGAGGAAATGGAACCTCTATCTGCCAGTCA
 GAAGATACAAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCT
 CTGGGCTGTGGAGTATGTGGGGAACATGACCTGCATGCCATGTGGAAGGGGGCACTCGG
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACAGCTCCACCTACTCCTTTTC
 TCCCCAAAACAATACCCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
 GCCTGGTGAGGAACCCGTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT
 GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
 TGACCTTGGAGAGGCCATCCTATTTGATTGTCTGCTGATTCTCATCCCCCAACACCTACT
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCCTCGCTTAGAAGTT
 GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTTACAACAACATAAC
 CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
 CACAGAAAGGAAAAATCATTTGTCACTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT
 ATATCCATGTGTCTTCTCTTCCATGGAAAAAATATCAACCCACAAAGTTATAAAAACAGAA
 ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
 CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
 ATTTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
 GTATGAAGTTATTTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGT**G**AACTTTCATGG
 GCTAAACAGTACATTCGAGTGAAATCTGAAGAAACATTTTAAAGAAAAACAGTGGAAAAAGT
 ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCTTTTACA
 TGCAGAATAGAGGCATTTATGCAAAATTGAACCTGCAGGTTTTTCAGCATATACAAATGTCTT
 GTGCAACAGAAAAACATGTTGGGGAATATTCCTCAGTGGAGAGTCGTTTCTCATGCTGACGG
 GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTGTATGAAATATCTCTACAAACCTCA
 ATTAGTTCTACTCTACACTTTCCTACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
 TGTGGAACCTTTACATTGTTTCGATTTTTCAGCAGACTTGTGTTTATTAATTTTATTAGTG
 TTAAGAAATGCTAAATTTATGTTTCAATTTTATTTCCAATTTCTATCTTGTTATTGTACAA
 CAAAGTAATAAGGATGTTGTCAAAAAACAAACTATGCCTTCTCTTTTTCATTAATCACC
 AGTAGTATTTTTCAGAAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGCTTTATTTTAA
 TTTTTCAGGAAAGATGGATTCAAATAAATTATCTGTTTGTCTTTTAAAAA

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FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQI IWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSLVRNPVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVGVEFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTV IITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 113

GCAAGCGCGGAAATGCGGCCCTCCGGGAGTCTTGCAGTTCCTTGGCAGTCTTGGTGTCTGTT
GCTTTGGGGTGCTCCCTGGAGCAGCGGGCGGGGAGCAACGTTTCGCGTCACTACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAAATTTATGCCCGTGGTGCCCTGTCT
TGTCAAATCTTCAACCGGAAATGGGAAAGTTTGTGTAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGTCTC
TTCCTACTATTTATCATGTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTCTGATGAGTAGTATGTCAGCACTCTTTTTCAGCTATCTATGTGGA
TCAGGACGTCGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGTCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCCTTGTCTTCAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAGAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAAGCTGAAAGTAAAGAAGGAACAACAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAAACAGAAGATTGATCATTTTGTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTTCAGTCTAGATTGTCAATAATTTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTAAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTATGATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAAATTACATTTCCCAAGTATTGCAATTAT
TGAGGTATTTAAGAAGATTATTTAGAGAAAAATATTCTCATTTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAAGATATTTCCCATAAATGGGAAGTTTGGCCATTGTCTCAAG
AAATGTGTATTTTCACTGACAATTTCTGTGGTCTTTTTAGAGGTATATTCAAAATTTCTCTGT
ATTTTTAGGTTATGCAACTAATAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTTTAAAGTTCATGGTATTCTCTTGATT
CAACAAAGTTTGATTTTCTCTGTGATTTTCTTACTTACTATGGGTTACATTTTATTTT
CAAATTTGGATGATAATTTCTTGAAACATTTTATGTTTTAGTAAACAGTATTTTTTGT
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAACTCTGTGTAATTTAAAT
TTGGCCACTTTTTTCAGATTTTACATCATCTTGTCTGAACCTTCAACTTGAATTTGTTTTT
TTTCTTTTGGATGTGAAGGTGAACATTTCTGATTTTTGTCTGATGTGAAAAAGCCTTGGA
TTTTCAATTTTGAATTTCAAAGAAGCTTAATATAAAAAGTTTGCACTTCTACTCAGGAAAAAG
CATCTTCTGTATATGCTTTAAATGTATTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTATATTTTTTAAAGACAA
ACTTCATATTATCCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGATTTTACAGGTA
GTCAGTAGGATGGAACATTTTAGTGATTTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACTTAAAGAAGGGGAAATCATAAATACAATGAATCAACTGACCATTACGCTAGTAGAC
AATTTCTGTAATGTCCCTTCTTCTAGGCTCTGTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCAT
AAAGAGTTTGATGTGTAACCTGTGATGCTTGAATAATATCTTAAGCACAAAAATAACCT
TTCTAACCACTTCATTAAGCTGAAAAAATAAAAAA

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QUESTIONS

Signal sequence:

Transmembrane domain:

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCCTT
 CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTTGGAAGAGCGGG
 AAGGTCCTGGCCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
 ATTGCTGATGGCCCTGGTTTGGTGTCCCTGAGCTGTGTGCAGGCCGAATTCTTACCTCTATTG
 GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAAGCTTTC AAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCCTTGAC
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGTAATGCCTACAAACTTGG
 TGAAGCGGCTAAACACAGACTGGCCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
 GGTTTTATCGCCAACTCTCTGTGCAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACCTTCAGGAACCAAGTAC CAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATCGCGGGGAGGAGGCCACCAACCAAGTCA CAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCGCCTGCTC
 TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAACAATCAGACAGAAGCTGAGCTAGCAACCC CAGAAGGCA
 TCTATGAGAGGCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAGAGGCTTTTCTGTAGGTACCCACATGGCAA
 CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
 TCCTCAGGTACTACGATGTCATGCTGTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTCACTGTGCGCAGCTA
 CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTTGTACAGGTTGCAAAAT
 TATGGAGTGGGAGGACAGTATGAACCGCACCTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGATAGAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCCTAAGAAGGGTACAGCTGTG
 TTTCTGTGTAACCTCTTTCGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCTGCCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCTTCTCTGGTC
 CTTACGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTTATCAGGCT
 GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
 GTGACTGAAGTCCCAGCCCTTCCATT CAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTAT
 GGCATTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCTACCAGAAAAA

FIGURE 117

GCAGTATTGAGTTTACTTCCCTCTCTTTTGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCAATTATTACCGTTTGTGGCTGGGGGTTAGTTCGCACACCTTCACAGTTGAAGAGCAGGCAGAGGAGTTGTGA
AGACAGGACAATCTTCTGGGGATCGTGGCTCTGGAAGCCAGCGGCCCTTGTCTGTCTTGTGGCCCTATTGACCC
CAGGTTCTCTGTTTAAACTGAAAGCCTACTACTGGCCTGGTGGCCATCAATCCATTGATCTCTGGAGGCTGTGCC
CCTGGGGCACCCCTTGGCAGGGCTACCACTATGCGACTGAGCTCCTGTGTGGCTCTGCTCGGGCCAGCGCTTC
CCCTCATCTTAGGGCTCTCTCTGGGGTGCAGCCTGAGCCTCTCTGCGGGTTTCTCGGATCCAGGGGGAGGGAGAAG
ATCCCTCTGTTCGAGCTGTAGGGGAGCGGAGGAGGGCCACAGAATCCAGATTTCGAGAGCTCGGCTAGACCAAAGTG
ATGAGACATCTCAAACCCCGGATTGTCCCTCACTACAGGGACCCCAACAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCTGAGCGGTGTCTGGTGGCTGTCTGTGACCTCCCGAGCTACACTGTGCCA
CTTTGGCCGTGGCTGTGAACCCATCGGTGGCCCATCACTTCCCTCGGTTACTTCACTTCACTGGGCAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTACAGAGACCTTGC
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTCTTCTCATGTGACGAGTACACATATGTGACAGGCC
CCCGCTTGGCAGCCCTTGTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTCATTG
GCGCAGGCGAGCAGGCCCGGTACTGTCTATGGGGCTTTGGCTACTGTTGTCTCAGGAGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCCGAGGAGACATCTCAGTGCCCTCTGACAGTGGCTTGGACGCTGCCTCATGT
ACTCTCTGGGCGTCGGCTGTGTCTACAGCACCAAGGGCAGCAGTATCGCTCATTTGAACTGGCCMAAAATAGGG
ACCCCTGAAGAAGGAGGAGCTCGGCTTTCCTGAGTGCTCTCGCCGTGCACCTGTCTCCGAAGGTACCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAAGAACACTGCAGGCTCAGAG
TCCGGAACCTGACCGTGCTGACCCCCAAGGGGAGGAGCGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCTTTCA
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACTTCTCTGTGCAGATGGGG
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGCTATCAGCCCCGCTCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAGC
GGGCGATGGAGTACACCTTGGACTGCTGTTGGAAATGTGTGACACAGCGTGGGCACCGGGGGCCCTGGCTGCA
GGGTGAGCCTGCTGCGCCACTGAGCCGGGTGGAATCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC
AGCTGTGTCTGCCACTCCTGGTGGCTGAAGCTGCTGACGCCCGGCTTTCCTCGAGGCGTTTGCAGCCAAATGCTC
TGGAGCCACGAGAATGCAATTGCTCAACCTGTTGCTGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG
ACCCATTCTTGGGGTGAAGGCTGACAGCAGCGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGTGACGTGCTCTCGAAGAAGCACCTGTGGACACTCTCT
TCTTCTTACCACCGTGTGGACAAGGCTGGGCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
GGCAGGCCCTCTTCCAGTCCATTTCCAGGAGTCAATCCTGCCCTGTCAACACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTCTCTGGTGTGACCCCTCCCGGGGGGCTCTATAGGGGGGAGATTTC
ACCGGCGAGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACTGGCGGGCCGAGCCCGGCTGGCAGGTGAAC
TGGCAGGCGCAGGAAGAGGAGGAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCCTCCGGTTCTCAGGGCTCC
ACCTCTTCTGGGCTGAGGACAGGCTGGTGCAGAAGTTCTCCTGCGAGACTCAGCCACGGCTCAGTGAAG
AACTCTACCAACGCTGCGCGCTCAGCAACCTGGAGGGGCTAGGGGGCGCTGCCAGCTGGCTATGGCTCTCTTTG
AGCAGGAGCAGGCGAATAGCACTTAGCCCGCTGGGGCCCTAACCTCATTAATCTTCCTTTGTCTGCCCTCAGCC
CCAGGAAGGCGAAGCAAGATGTTGGACAGATAGAGAATTTGTTGCTGTATTTTAAATATGAAATGTTATTAA
ACATGTCTTCTGCC

09904877.071201

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEGEDPCVEAVGERGGPQNPDSSRARLD
QSEDEFKPRIVPYRDPNPKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTQGQGARAPAGMQVVS HGDERP AWMSETLRHLHTHFGADYDWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHFVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQGASRADVGDALETALEQLNRRYQPRLRFQKQRLNNGYR
RFDPARGMEYTLDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVLVPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG
TRLAWLAVRAEAPSOVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFPP
VHFQEFNPALSPQRSPPGPPGACGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDFLRFSGHLFRAVEPGLVQKFSRLDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQA NST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAAAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAAGCAG
AGTTCCTCAGTTCGAAAATGTTAAAGTGTTGAGTCAATTAATATGGACCAAATGACATG
TGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTTAA
AAAAGGATCCATCAGACCTTTTCTATCTAGGCCCACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTCCAGATATGGCTGTTACTTTTAATGGACTGACTCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTTAAATGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTTGGAAGAAGTGTTTTAAGAATAATAATTTGCAAATAAACTATTATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTCTCT
AAGCCTCCCCAAGTTCCAATGGATTGGCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVM LGSIFCALITMLGHIRIGHGNRMHHEHHHLQAPNKEDILKISEDERME
LSKSPRVYCIILVKPKD VSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHGTIKSGDLEYVGMMEG
IVLSVESMKRLNLSLLNIPEKCP EQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDV FNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAF GHI FNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAAACAAAAACCAAAGAGAGAGAGAAAAATGAATTTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCTATTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCACTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAAAATGAGAGAGTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAA
AA
AAAAA

09504877-071201

DEPARTMENT OF THE ARMY

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
 PRIEWKKIQDEQTTYVFDNKKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAVRNDRK
 EIDEIVIELTVQKVPVTPVPCVRPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRA
 NPRFRNSSFHLNSETGLTVFIAVHKDGSQQYCIASNDAGSARCEEQMEVYDLNTGGIIGG
 VLVVLAVLALITGLGICACRYRGYFINNKQDGESYKNPKGPKGVNYIRTEEGDFRHKSSSFI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267